

SEQUENCE LISTING

<110> Koffas, Mattheos
Odom, James M
Schenzle, Andreas J

<120> DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

<130> CL1596 US NA

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<150> 60/229,858

<151> September 1, 2000

<160> 81

<170> Microsoft Office 97

<210> 1

<211> 1434

<212> DNA

<213> METHYLOMONAS SP.

<400> 1

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cgatatTTTta atcgacaagc gattcagatc atcatcaaaa tggcggccgc taacgggttt   240
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gatcccgtgg ccgattacgc cgaattgatg gcccgattt tcgatttcga cctgatcaag   600
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ttgcccgcca aaacctgggg cgattacagc gtcaaattcg ccgacgaatt cagctatacc  1380
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<210> 2

<211> 545

<212> PRT

<213> METHYLOMONAS SP.

<400> 2

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 Gly Tyr Leu Glu Asn Phe Val Gln Ser Ile Phe Asn Ser Leu Glu Asp
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 Phe Gln Gly Lys Ile Leu Val Leu Gly Gly Asp Gly Arg Tyr Phe Asn
 50 55 60
 Arg Gln Ala Ile Gln Ile Ile Ile Lys Met ala Ala Ala Asn Gly Phe
 65 70 75 80
 Gly Glu Leu Ile Ile Gly Gln Gly Gly Leu Leu Ser Thr Pro Ala Ala
 85 90 95
 Ser Asn Val Ile Arg Lys Tyr Arg Ala Phe Gly Gly Ile Ile Leu Ser
 100 105 110
 Ala Ser His Asn Pro Gly Gly Pro Asp Glu Asp Phe Gly Ile Lys Tyr
 115 120 125
 Asn Val Gly Asn Gly Gly Pro Ala Pro Glu Lys Phe Thr Asp Ala Leu
 130 135 140
 Phe Glu Asn Ser Lys Thr Ile Thr Ser Tyr Gln Met ala Glu Ile Asp
 145 150 155 160
 Asp Ile Asp Leu Asp Ser Val Gly Asp Val Gln Ile Asp Gly Ile Thr
 165 170 175
 Ile Arg Ile Ile Asp Pro Val Ala Asp Tyr Ala Glu Leu Met ala Arg
 180 185 190
 Ile Phe Asp Phe Asp Leu Ile Lys Gln Ser Ile Ala Ala Gly Leu Ile
 195 200 205
 Thr Leu Arg Phe Asp Ala Met His Ala Ile Thr Gly Pro Tyr Ala Lys
 210 215 220
 His Ile Leu Glu Asp Val Leu Gly Ala Ala Pro Gly Ser Val Phe Asn
 225 230 235 240
 Ala Val Pro Leu Glu Asp Phe Gly Gly Gly His Pro Asp Pro Asn Met
 245 250 255
 Ala His Ala His Glu Leu Thr Glu Ile Met Phe Gly Pro Asn Pro Pro
 260 265 270
 Val Phe Gly Ala Ala Ser Asp Gly Asp Gly Asp Arg Asn Met Ile Met
 275 280 285
 Gly Ala Asn Ile Phe Val Thr Pro Ser Asp Ser Leu Ala Ile Met ala
 290 295 300
 Ala Asn Ala Gln Leu Ile Pro Ala Tyr Ala Lys Gly Ile Ser Gly Val
 305 310 315 320
 Ala Arg Ser Met Pro Thr Ser Gln Ala Val Asp Arg Val Ala Asp Lys
 325 330 335

Leu Ser Leu Pro Cys Tyr Glu Thr Pro Thr Gly Trp Lys Phe Phe Gly
 340 345 350
 Asn Leu Leu Asp Ala Asp Lys Ile Thr Leu Cys Gly Glu Glu Ser Phe
 355 360 365
 Gly Ser Gly Ser Asn His Val Arg Glu Lys Asp Gly Leu Trp Ala Val
 370 375 380
 Leu Phe Trp Leu Asn Leu Leu Ala Arg Lys Arg Gln Pro Ala Glu Asp
 385 390 395 400
 Ile Val Arg Glu His Trp Gln Lys Tyr Gly Arg Asp Ile Tyr Cys Arg
 405 410 415
 His Asp Tyr Glu Ala Val Asp Ala Asp Ile Ala Asn Gly Ile Val Glu
 420 425 430
 Gln Leu Arg Asn Gln Leu Pro Ser Leu Pro Gly Lys Thr Trp Gly Asp
 435 440 445
 Tyr Ser Val Lys Phe Ala Asp Glu Phe Ser Tyr Thr Asp Pro Val Asp
 450 455 460
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 465 470 475 480
 Ser Arg Ile Val Phe Arg Leu Ser Gly Thr Gly Thr Val Gly Ala Thr
 485 490 495
 Leu Arg Ile Tyr Leu Glu Arg Tyr Glu Arg Asp Val Arg Asn His Asp
 500 505 510
 Gln Asp Pro Gln Val Ala Leu Ala Glu Leu Ile Glu Ile Ala Glu Gln
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 Leu Cys Gln Val Lys Gln Arg Thr Gly Arg Thr Glu Pro Ser Val Ile
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<210> 3
 <211> 1387
 <212> DNA
 <213> METHYLOMONAS SP.

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 ggttcacaca aaaataatat gtccaaatta atcaactctg ccgaatggaa cgccgtcaaa 180
 caacatcatc aagaaattgc tggtaaattt tgcataaaag aggcttttgc caaagatccc 240
 cagcgtttgc ataaattctc cgtcaccttt aacgacatat tattagacta ttccaaaaaac 300
 ctgatcgacg agcgcaccat gcccttgctg atcgcatggg caaagcgggc agacttgccg 360
 gagaaaacgg aagcgatgtt ttccggctcc atcatcaaca ccaccgaaaa acgcgcgggt 420
 ttgcataaccg cgctgcgaaa ccgtagcaat acgcccgttt tcttccgcgg ccaggatgtc 480
 atgccggaat tcaacaagggt tctggcaaaa atgcggggtt tcgtggaaca ggtgcgttcg 540
 ggccaatgga cgggctatag cggcaaggcc attaccgata tcgtcaacat cggcattggc 600

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<210> 4

<211> 592

<212> PRT

<213> METHYLOMONAS SP.

<400> 4

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Lys Ala Ser Glu Asp Ser Leu Ser Gly Ser His Lys Asn Asn Met Ser
      35              40              45

Lys Leu Ile Asn Ser Ala Glu Trp Asn Ala Val Lys Gln His His Gln
      50              55              60

Glu Ile Ala Gly Lys Phe Cys Met Lys Glu Ala Phe Ala Lys Asp Pro
      65              70              75              80

Gln Arg Phe Asp Lys Phe Ser Val Thr Phe Asn Asp Ile Leu Leu Asp
      85              90              95

Tyr Ser Lys Asn Leu Ile Asp Glu Arg Thr Met Pro Leu Leu Ile Ala
      100             105             110

Leu Ala Lys Arg Ala Asp Leu Arg Glu Lys Thr Glu Ala Met Phe Ser
      115             120             125

Gly Ser Ile Ile Asn Thr Thr Glu Lys Arg Ala Val Leu His Thr Ala
      130             135             140

Leu Arg Asn Arg Ser Asn Thr Pro Val Phe Phe Arg Gly Gln Asp Val
      145             150             155             160

Met Pro Glu Ile Asn Lys Val Leu Ala Lys Met Arg Val Phe Val Glu
      165             170             175

Gln Val Arg Ser Gly Gln Trp Thr Gly Tyr Ser Gly Lys Ala Ile Thr
      180             185             190

Asp Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Lys Met
      195             200             205

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Ala Phe Tyr Glu His Lys Ile Phe Val Gln Gly Val Ile Trp Asn Ile
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Asn Ser Phe Asp Gln Met Gly Val Glu Leu Gly Lys Val Leu Ala Lys
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Ala Ile Leu Pro Glu Leu Lys Asn Asp Asp Ile Ile Ala Ser His Asp
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Ser Ser Thr Asn Gly Leu Ile Asn Thr Tyr Lys Arg Leu Arg Lys Ala
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<210> 5
<211> 1311
<212> DNA
<213> METHYLOMONAS SP.

<400> 5
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ggcggcttgg cgccttggtt gaattccgca atcggtagtt tgatcgaacg ttataccgaa 180
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gcagcattcc tggccagaaa taattacgga ctgaccgtca ttggtttacc taaaaccgtc 540
gataacgacg tatttccgat caagcaatca ctagggtgctt ggactgccgc cgagcaaggc 600
gcgcgttatt tcatgaacgt ggtggccgaa aacaacgcca acccagcat gctgatcgta 660
cacgaagtga tgggccgtaa ctgcggctgg ctgaccgctg caaccgcgca ggaatatcgc 720
aaattactgg accgtgccga gtggttgccg gaattgggtt tgactcgtga atcttatgaa 780
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<210> 6
<211> 437
<212> PRT
<213> METHYLOMONAS SP.

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Lys Lys Val Ala Ile Leu Thr Ala Gly Gly Leu Ala Pro Cys Leu Asn
35 40 45

Ser Ala Ile Gly Ser Leu Ile Glu Arg Tyr Thr Glu Ile Asp Pro Ser
 50 55 60
 Ile Glu Ile Ile Cys Tyr Arg Gly Gly Tyr Lys Gly Leu Leu Leu Gly
 65 70 75 80
 Asp Ser Tyr Pro Val Thr Ala Glu Val Arg Lys Lys Ala Gly Val Leu
 85 90 95
 Gln Arg Phe Gly Gly Ser Val Ile Gly Asn Ser Arg Val Lys Leu Thr
 100 105 110
 Asn Val Lys Asp Cys Val Lys Arg Gly Leu Val Lys Glu Gly Glu Asp
 115 120 125
 Pro Gln Lys Val Ala Ala Asp Gln Leu Val Lys Asp Gly Val Asp Ile
 130 135 140
 Leu His Thr Ile Gly Gly Asp Asp Thr Asn Thr Ala Ala Ala Asp Leu
 145 150 155 160
 Ala Ala Phe Leu Ala Arg Asn Asn Tyr Gly Leu Thr Val Ile Gly Leu
 165 170 175
 Pro Lys Thr Val Asp Asn Asp Val Phe Pro Ile Lys Gln Ser Leu Gly
 180 185 190
 Ala Trp Thr Ala Ala Glu Gln Gly Ala Arg Tyr Phe Met Asn Val Val
 195 200 205
 Ala Glu Asn Asn Ala Asn Pro Arg Met Leu Ile Val His Glu Val Met
 210 215 220
 Gly Arg Asn Cys Gly Trp Leu Thr Ala Ala Thr Ala Gln Glu Tyr Arg
 225 230 235 240
 Lys Leu Leu Asp Arg Ala Glu Trp Leu Pro Glu Leu Gly Leu Thr Arg
 245 250 255
 Glu Ser Tyr Glu Val His Ala Val Phe Val Pro Glu Met ala Ile Asp
 260 265 270
 Leu Glu Ala Glu Ala Lys Arg Leu Arg Glu Val Met Asp Lys Val Asp
 275 280 285
 Cys Val Asn Ile Phe Val Ser Glu Gly Ala Gly Val Glu Ala Ile Val
 290 295 300
 Ala Glu Met Gln Ala Lys Gly Gln Glu Val Pro Arg Asp Ala Phe Gly
 305 310 315 320
 His Ile Lys Leu Asp Ala Val Asn Pro Gly Lys Trp Phe Gly Glu Gln
 325 330 335
 Phe Ala Gln Met Ile Gly Ala Glu Lys Thr Leu Val Gln Lys Ser Gly
 340 345 350
 Tyr Phe Ala Arg Ala Ser Ala Ser Asn Val Asp Asp Met Arg Leu Ile
 355 360 365

Lys Ser Cys Ala Asp Leu Ala Val Glu Cys Ala Phe Arg Arg Glu Ser
 370 375 380
 Gly Val Ile Gly His Asp Glu Asp Asn Gly Asn Val Leu Arg Ala Ile
 385 390 395 400
 Glu Phe Pro Arg Ile Lys Gly Gly Lys Pro Phe Asn Ile Asp Thr Asp
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 Val Glu Val Ser His
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<210> 7
 <211> 1360
 <212> DNA
 <213> METHYLOMONAS SP.

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 gcggccggcg gcatgagctt attgatacac gaactgctgg atcacggctt gttgcacggc 1140
 gacatcctga ccataggcga ccagcgcggc atggcccaat acagtcaagt accgacgctg 1200
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 ggccgcggcg tatccaagat ttccgccgtc tccgaagatc 1360

<210> 8
 <211> 618
 <212> PRT
 <213> METHYLOMONAS SP.

<400> 8
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 Leu Glu Lys Val Thr Glu Gln Val Ile Ala Arg Ser Arg Glu Thr Arg
 20 25 30

Ala	Ala	Tyr	Leu	Lys	Arg	Ile	Glu	Ala	Ala	Ile	Ala	Glu	Gly	Pro	Gln		
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Arg	Asn	Lys	Leu	Pro	Cys	Ala	Asn	Leu	Ala	His	Gly	Phe	Ala	Val	Cys		
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Ser	Ala	Ile	Glu	Lys	Glu	Glu	Leu	Ser	His	Gly	Pro	Lys	Pro	Asn	Val		
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Gly	Ile	Ile	Ser	Ala	Tyr	Asn	Asp	Met	Leu	Ser	Ala	His	Glu	Pro	Tyr		
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Lys	Asp	Tyr	Pro	Ala	Leu	Ile	Lys	Gln	Ala	Val	Arg	Glu	Ala	Gly	Gly		
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Val	Ala	Gln	Phe	Ala	Gly	Gly	Val	Pro	Ala	Met	Cys	Asp	Gly	Val	Thr		
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Gln	Gly	Met	Pro	Gly	Met	Glu	Leu	Ser	Leu	Phe	Ser	Arg	Asp	Val	Ile		
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Ala	Met	Ser	Thr	Ala	Ile	Gly	Leu	Ala	His	Asn	Met	Phe	Asp	Ala	Ala		
	145				150					155					160		
Leu	Tyr	Leu	Gly	Val	Cys	Asp	Lys	Ile	Val	Pro	Gly	Leu	Leu	Ile	Gly		
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Ala	Leu	Ser	Phe	Gly	His	Leu	Pro	Ala	Val	Phe	Leu	Pro	Ala	Gly	Pro		
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Tyr	Ala	Glu	Gly	Lys	Ile	Gly	Glu	Lys	Glu	Leu	Leu	Glu	Ser	Glu	Ala		
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Lys	Ser	Tyr	His	Ser	Pro	Gly	Thr	Cys	Thr	Phe	Tyr	Gly	Thr	Ala	Asn		
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Ser	Phe	Ile	Asn	Pro	Tyr	Thr	Pro	Leu	Arg	Asp	Glu	Leu	Thr	Lys	Ala		
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Pro	Ile	Ala	His	Val	Ile	Asp	Glu	Lys	Ala	Ile	Ile	Asn	Ala	Ile	Ile		
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Ala	Leu	Ser	Lys	Val	Ile	Pro	Leu	Leu	Thr	Lys	Ile	Tyr	Pro	Asn	Gly		
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 Ile His Glu Leu Leu Asp His Gly Leu Leu His Gly Asp Ile Leu Thr
 370 375 380
 Ile Gly Asp Gln Arg Gly Met ala Gln Tyr Ser Gln Val Pro Thr Leu
 385 390 395 400
 Gln Asp Gly Gln Leu Gln Trp Gln Pro Gly Pro Thr Ala Ser Arg Asp
 405 410 415
 Pro Glu Ile Ile Ala Ser Val Ala Lys Pro Phe Ala Ala Gly Gly Gly
 420 425 430
 Leu His Val Met His Gly Asn Leu Gly Arg Gly Val Ser Lys Ile Ser
 435 440 445
 Ala Val Ser Glu Asp His Gln Val Val Thr Ala Pro Ala Met Val Phe
 450 455 460
 Asp Asp Gln Leu Asp Val Val Ala Ala Phe Lys Arg Gly Glu Leu Glu
 465 470 475 480
 Lys Asp Val Ile Val Val Leu Arg Phe Gln Gly Pro Lys Ala Asn Gly
 485 490 495
 Met Pro Glu Leu His Lys Leu Thr Pro Val Leu Gly Val Leu Gln Asp
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 Arg Gly Phe Lys Val Gly Leu Leu Thr Asp Gly Arg Met Ser Gly Ala
 515 520 525
 Ser Gly Lys Val Pro Ser Ala Ile His Met Trp Pro Glu Cys Ile Asp
 530 535 540
 Gly Gly Pro Leu Ala Lys Val Arg Asp Gly Asp Ile Ile Val Met Asn
 545 550 555 560
 Thr Gln Thr Gly Glu Val Asn Val Gln Val Asp Pro Ala Glu Phe Lys
 565 570 575
 Ala Arg Val Ala Glu Pro Asn His Ala Thr Gly His His Phe Gly Met
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<210> 9

<211> 1477

<212> DNA

<213> METHYLOMONAS SP.

<400> 9

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tcattataacc gtttggaaaa acacaatctg ctcgagcccg atacgcgcat catcggcgta 180
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accgaaagca cgaccgaaac tttcgtcgcg atccgcgtgg atatcgataa ctggcgctgg 1020
gccggtgtcc cgttttacat gcgtaccggc aaacgcacgc ccaacaaacg caccgagatt 1080
gtggtcaatt tcaagcaatt gccgcacaa atcttcaagg acagttttca tgaactgccg 1140
gccaataaac tggtcattca tttgcaaccg aacgaagggg tggatgtcat gatgttgaac 1200
aaggtgccgg gcatagacgg caacatcaag ttgcaacaga ccaaactgga tttgagcttt 1260
tccgaaacct tcaagaaaaa ccgaattttc ggcggtacg aaaaactgat tctggaagcc 1320
ctgcgcggca acccgacgct gtttttgagc cgcgaggaaa tagaacaagc ctggacctgg 1380
gtcgattcga ttcaggatgc ctggcaacac aaccacacgc caccacaaacc ctatcccgcg 1440
ggtagctggg gtccagtggc atcggtcgca ttactgg 1477

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<210> 10

<211> 501

<212> PRT

<213> METHYLOMONAS SP.

<400> 10

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Met ala Leu Gly Phe Leu Leu Arg Ser Pro Lys Asp Met Thr Lys Asn
  1                      5                      10                      15

Ile Thr Tyr Lys Pro Cys Asp Leu Val Ile Tyr Gly Ala Leu Gly Asp
      20                      25                      30

Leu Ser Lys Arg Lys Leu Leu Ile Ser Leu Tyr Arg Leu Glu Lys His
      35                      40                      45

Asn Leu Leu Glu Pro Asp Thr Arg Ile Ile Gly Val Asp Arg Leu Glu
      50                      55                      60

Glu Thr Ser Asp Ser Phe Val Glu Ile Ala His Lys Ser Leu Gln Ala
      65                      70                      75                      80

Phe Leu Asn Asn Val Ile Asp Ala Glu Ile Trp Gln Arg Phe Ser Lys
      85                      90                      95

Arg Leu Ser Tyr Leu Lys Ile Asp Leu Thr Gln Pro Glu Gln Tyr Lys
      100                     105                     110

Gln Leu His Thr Val Val Asp Ala Glu Lys Arg Val Met Val Asn Tyr
      115                     120                     125

Phe Ala Val Ala Pro Phe Leu Phe Lys Asn Ile Cys Gln Gly Leu His
      130                     135                     140

Asp Cys Gly Val Leu Thr Ala Glu Ser Arg Met Val Met Glu Lys Pro
      145                     150                     155                     160

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Ile	Gly	His	Asp	Leu	Lys	Ser	Ser	Lys	Glu	Ile	Asn	Asp	Val	Val	Ala		
				165					170					175			
Asp	Val	Phe	His	Glu	Asp	Gln	Val	Tyr	Arg	Ile	Asp	His	Tyr	Leu	Gly		
			180					185					190				
Lys	Glu	Thr	Val	Leu	Asn	Leu	Leu	Ala	Leu	Arg	Phe	Ala	Asn	Ser	Ile		
		195					200					205					
Phe	Thr	Thr	Asn	Trp	Asn	His	Asn	Thr	Ile	Asp	His	Ile	Gln	Ile	Thr		
	210					215					220						
Val	Gly	Glu	Asp	Ile	Gly	Ile	Glu	Gly	Arg	Trp	Glu	Tyr	Phe	Asp	Lys		
225					230				235						240		
Thr	Gly	Gln	Leu	Arg	Asp	Met	Leu	Gln	Asn	His	Leu	Leu	Gln	Ile	Leu		
				245					250					255			
Thr	Phe	Val	Ala	Met	Glu	Pro	Pro	Ala	Asp	Leu	Ser	Ala	Glu	Ser	Ile		
			260					265					270				
His	Met	Glu	Lys	Ile	Lys	Val	Leu	Lys	Ala	Leu	Arg	Pro	Ile	Thr	Val		
		275					280					285					
Arg	Asn	Val	Glu	Glu	Lys	Thr	Val	Arg	Gly	Gln	Tyr	Thr	Ala	Gly	Phe		
	290					295					300						
Ile	Lys	Gly	Lys	Ser	Val	Pro	Gly	Tyr	Leu	Glu	Glu	Glu	Gly	Ala	Asn		
305					310					315					320		
Thr	Glu	Ser	Thr	Thr	Glu	Thr	Phe	Val	Ala	Ile	Arg	Val	Asp	Ile	Asp		
				325					330					335			
Asn	Trp	Arg	Trp	Ala	Gly	Val	Pro	Phe	Tyr	Met	Arg	Thr	Gly	Lys	Arg		
			340					345					350				
Thr	Pro	Asn	Lys	Arg	Thr	Glu	Ile	Val	Val	Asn	Phe	Lys	Gln	Leu	Pro		
		355					360					365					
His	Asn	Ile	Phe	Lys	Asp	Ser	Phe	His	Glu	Leu	Pro	Ala	Asn	Lys	Leu		
	370					375					380						
Val	Ile	His	Leu	Gln	Pro	Asn	Glu	Gly	Val	Asp	Val	Met	Met	Leu	Asn		
385					390					395					400		
Lys	Val	Pro	Gly	Ile	Asp	Gly	Asn	Ile	Lys	Leu	Gln	Gln	Thr	Lys	Leu		
				405					410					415			
Asp	Leu	Ser	Phe	Ser	Glu	Thr	Phe	Lys	Lys	Asn	Arg	Ile	Phe	Gly	Gly		
			420					425					430				
Tyr	Glu	Lys	Leu	Ile	Leu	Glu	Ala	Leu	Arg	Gly	Asn	Pro	Thr	Leu	Phe		
	435						440					445					
Leu	Ser	Arg	Glu	Glu	Ile	Glu	Gln	Ala	Trp	Thr	Trp	Val	Asp	Ser	Ile		
	450					455					460						
Gln	Asp	Ala	Trp	Gln	His	Asn	His	Thr	Pro	Pro	Lys	Pro	Tyr	Pro	Ala		
465					470					475					480		

Gly Ser Trp Gly Pro Val Ala Ser Val Ala Leu Leu Ala Arg Asp Gly
485 490 495

Arg Ala Trp Glu Glu
500

<210> 11
<211> 984
<212> DNA
<213> METHYLOMONAS SP.

<400> 11
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gacatccagg cgatcgaaac cttcaagccg cgcgatgcaa cgaccaaccc gtctttgatc 120
accgccgcgg cgcaaatgcc gcaatatcaa ggcatcggtg acgacacctt gaaagggtgcg 180
cgtgcgacgt tgggtgccag cgcttcggct gccgaggtgg cttcattggc gttcgatcgt 240
ttggcggttt ctttcggttt gaaaatcctg gaaatcatcg aaggctcgctg ttccaccgag 300
gttgatgcgc gtttgtctta tgacaccgaa ggcaactattg ccaaaggccg ggatctgatc 360
aaacaatacg aagctgcagg tgtttccaaa gagcgcgtac tgatcaaaat tgccgcgacc 420
tgggaaggca tccaggcggc tgccgttttg gaaaaagaag gtattcacac caacttgacc 480
ctgttggttcg gtctgcacca ggcgattgct tgtgccgaaa acggcattac cctgatttct 540
ccgtttgtcg gccgtattct ggactggtac aaaaaagaca ctggccgcga ctcttatcct 600
tccaacgaag atcctggcgt attgtctgta actgaagttt ataactacta caaaaaattt 660
ggttataaaa ctgaagtcac gggcgcgagc ttccgtaaca tcggcgaaat caccgaattg 720
gcgggttgcg atctgttgac catcgcgctt tctctgctgg ccgaactgca atccgttgaa 780
ggtgatttgc cagcgaactt ggaccctgca aaagcagccg gttcttcgat cgaaaaaatc 840
agcgttgaca aagcgacttt cgagcgcgtg cacgaagaaa accgcatggc caaagaaaaa 900
ctggccgaag gtatcgacgg ttttgcgaaa gcgttggaiaa ccttggaiaa attgttggcg 960
gatcggttgg ctgctctgga agca 984

<210> 12
<211> 328
<212> PRT
<213> METHYLOMONAS SP.

<400> 12
Met ala Arg Asn Leu Leu Glu Gln Leu Arg Glu Met Thr Val Val Val
1 5 10 15
Ala Asp Thr Gly Asp Ile Gln Ala Ile Glu Thr Phe Lys Pro Arg Asp
20 25 30
Ala Thr Thr Asn Pro Ser Leu Ile Thr Ala Ala Ala Gln Met Pro Gln
35 40 45
Tyr Gln Gly Ile Val Asp Asp Thr Leu Lys Gly Ala Arg Ala Thr Leu
50 55 60
Gly Ala Ser Ala Ser Ala Ala Glu Val Ala Ser Leu Ala Phe Asp Arg
65 70 75 80
Leu Ala Val Ser Phe Gly Leu Lys Ile Leu Glu Ile Ile Glu Gly Arg
85 90 95
Val Ser Thr Glu Val Asp Ala Arg Leu Ser Tyr Asp Thr Glu Gly Thr
100 105 110

Ile Ala Lys Gly Arg Asp Leu Ile Lys Gln Tyr Glu Ala Ala Gly Val
 115 120 125
 Ser Lys Glu Arg Val Leu Ile Lys Ile Ala Ala Thr Trp Glu Gly Ile
 130 135 140
 Gln Ala Ala Ala Val Leu Glu Lys Glu Gly Ile His Thr Asn Leu Thr
 145 150 155 160
 Leu Leu Phe Gly Leu His Gln Ala Ile Ala Cys Ala Glu Asn Gly Ile
 165 170 175
 Thr Leu Ile Ser Pro Phe Val Gly Arg Ile Leu Asp Trp Tyr Lys Lys
 180 185 190
 Asp Thr Gly Arg Asp Ser Tyr Pro Ser Asn Glu Asp Pro Gly Val Leu
 195 200 205
 Ser Val Thr Glu Val Tyr Asn Tyr Tyr Lys Lys Phe Gly Tyr Lys Thr
 210 215 220
 Glu Val Met Gly Ala Ser Phe Arg Asn Ile Gly Glu Ile Thr Glu Leu
 225 230 235 240
 Ala Gly Cys Asp Leu Leu Thr Ile Ala Pro Ser Leu Leu Ala Glu Leu
 245 250 255
 Gln Ser Val Glu Gly Asp Leu Pro Arg Lys Leu Asp Pro Ala Lys Ala
 260 265 270
 Ala Gly Ser Ser Ile Glu Lys Ile Ser Val Asp Lys Ala Thr Phe Glu
 275 280 285
 Arg Met His Glu Glu Asn Arg Met ala Lys Glu Lys Leu Ala Glu Gly
 290 295 300
 Ile Asp Gly Phe Ala Lys Ala Leu Glu Thr Leu Glu Lys Leu Leu Ala
 305 310 315 320
 Asp Arg Leu Ala Ala Leu Glu Ala
 325

<210> 13
 <211> 480
 <212> DNA
 <213> METHYLOMONAS SP.

<400> 13
 atggccgcgg gcggcggtggg cttgacgcaa ttgctgccag aactggccga agctattggt 60
 ccgacgagcc gatttcatgt gcaggtcatt ggtgacacgg tggaggacat cgttgcggaa 120
 gccaaacggc tacacgattt gcccgtcgac atagtgggtga aaattccggc gcatggcgcc 180
 ggactggcgg ccatacaagca gatcaagcgc cacgatattc cgggtgctggc gacagcgatt 240
 tacaacgtgc agcaagggtg gctggcggct ttgaacggcg ccgattatct ggcgccttat 300
 ctgaatcgcg tcgataacca ggggttttgac ggtattggcg tggtcgccga tctgcagagc 360
 ttgatcgacc ggtatcaaat gccacccaaa ctctggtag cgagcttcaa aaacgtacaa 420
 caggtgctgc aggtgttgaa actgggcgtg gcgtcggtag cgctgccttt ggacattgtg 480

<210> 14
 <211> 160
 <212> PRT
 <213> METHYLOMONAS SP.

<400> 14
 Met ala Ala Gly Gly Val Gly Leu Thr Gln Leu Leu Pro Glu Leu Ala
 1 5 10 15
 Glu Ala Ile Gly Pro Thr Ser Arg Phe His Val Gln Val Ile Gly Asp
 20 25 30
 Thr Val Glu Asp Ile Val Ala Glu Ala Lys Arg Leu His Asp Leu Pro
 35 40 45
 Val Asp Ile Val Val Lys Ile Pro Ala His Gly Ala Gly Leu Ala Ala
 50 55 60
 Ile Lys Gln Ile Lys Arg His Asp Ile Pro Val Leu Ala Thr Ala Ile
 65 70 75 80
 Tyr Asn Val Gln Gln Gly Trp Leu Ala Ala Leu Asn Gly Ala Asp Tyr
 85 90 95
 Leu Ala Pro Tyr Leu Asn Arg Val Asp Asn Gln Gly Phe Asp Gly Ile
 100 105 110
 Gly Val Val Ala Asp Leu Gln Ser Leu Ile Asp Arg Tyr Gln Met Pro
 115 120 125
 Thr Lys Leu Leu Val Ala Ser Phe Lys Asn Val Gln Gln Val Leu Gln
 130 135 140
 Val Leu Lys Leu Gly Val Ala Ser Val Thr Leu Pro Leu Asp Ile Val
 145 150 155 160

<210> 15
 <211> 1005
 <212> DNA
 <213> METHYLOMONAS SP.

<400> 15
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 ccggcggttca acgtcagcaa catggagcag gtacaggcca tcatgcaggc ggccgctgcc 120
 tgcgatagtc cagtgatcat gcaagggttc gccggcgcca accgctatgc cggcgaagtg 180
 tttctacggc atttgatatt ggccggccgtg gagcaatata cgcataattcc ggtcgatcatg 240
 caccgcgacc atgcacccac gcccgcacatc tgcgcgcaag ccatacaatc gggcttcagc 300
 tcggtgatga tggacgggttc gttgctggca gacatgaaaa ccccggttc ttttgcatac 360
 aacgtcgacg tcacccgcac cgtggtcaag atggcgcatg cctgcggcgt atcgggtggaa 420
 ggcgaaatcg gctgcctggg agcgctggag gccaaagtccg cgcaagatca cagccgtttg 480
 ctgaccgatc ccgacgaagc ggtcgaattc gtcgaacaga cccaggtcga tgccgtggcc 540
 gtggccatcg gcaccagcca cggcgccctat aaattcagca agccgcccac cggcgaagtg 600
 ctggtgatca gtcgattgaa agaactgcag caacgactgc caaataccca ttttgtgatg 660
 catggctcca gttcggtgcc gcaggattgg ttgaaaatca tcaacgatta tggcggcgat 720
 attccgaaa cctatggcgt gccggtcgaa gaaatcgctg aaggcataaa atatggtgtg 780
 cgcaaggtca acatcgatac cgacctgcgc atggcgctcca ccggcgcgat gcgcagggtt 840

ctggcccaac cggaaaacgc ctcggagcta gacgcgcgca agacctatca agccgccagg 900
gacgcaatgc aggcattatg ccaggctcgc tacgaagcgt tcggttcggc gggacatgcc 960
ggcaaaatca aaccggtttc actggcggca atggccaaac gctat 1005

<210> 16
<211> 335
<212> PRT
<213> METHYLOMONAS SP.

<400> 16
Met ala Leu Val Ser Leu Arg Gln Leu Leu Asp Tyr Ala Ala Glu His
1 5 10 15
Gly Phe Ala Val Pro Ala Phe Asn Val Ser Asn Met Glu Gln Val Gln
20 25 30
Ala Ile Met Gln Ala Ala Ala Ala Cys Asp Ser Pro Val Ile Met Gln
35 40 45
Gly Ser Ala Gly Ala Asn Arg Tyr Ala Gly Glu Val Phe Leu Arg His
50 55 60
Leu Ile Leu Ala Ala Val Glu Gln Tyr Pro His Ile Pro Val Val Met
65 70 75 80
His Arg Asp His Ala Pro Thr Pro Asp Ile Cys Ala Gln Ala Ile Gln
85 90 95
Ser Gly Phe Ser Ser Val Met Met Asp Gly Ser Leu Leu Ala Asp Met
100 105 110
Lys Thr Pro Ala Ser Phe Ala Tyr Asn Val Asp Val Thr Arg Thr Val
115 120 125
Val Lys Met ala His Ala Cys Gly Val Ser Val Glu Gly Glu Ile Gly
130 135 140
Cys Leu Gly Ala Leu Glu Ala Lys Ser Ala Gln Asp His Ser Arg Leu
145 150 155 160
Leu Thr Asp Pro Asp Glu Ala Val Glu Phe Val Glu Gln Thr Gln Val
165 170 175
Asp Ala Val Ala Val Ala Ile Gly Thr Ser His Gly Ala Tyr Lys Phe
180 185 190
Ser Lys Pro Pro Thr Gly Glu Val Leu Val Ile Ser Arg Leu Lys Glu
195 200 205
Leu Gln Gln Arg Leu Pro Asn Thr His Phe Val Met His Gly Ser Ser
210 215 220
Ser Val Pro Gln Asp Trp Leu Lys Ile Ile Asn Asp Tyr Gly Gly Asp
225 230 235 240
Ile Pro Glu Thr Tyr Gly Val Pro Val Glu Glu Ile Val Glu Gly Ile
245 250 255

Lys Tyr Gly Val Arg Lys Val Asn Ile Asp Thr Asp Leu Arg Met ala
 260 265 270
 Ser Thr Gly Ala Met Arg Arg Phe Leu Ala Gln Pro Glu Asn Ala Ser
 275 280 285
 Glu Leu Asp Ala Arg Lys Thr Tyr Gln Ala Ala Arg Asp Ala Met Gln
 290 295 300
 Ala Leu Cys Gln Ala Arg Tyr Glu Ala Phe Gly Ser Ala Gly His Ala
 305 310 315 320
 Gly Lys Ile Lys Pro Val Ser Leu Ala Ala Met ala Lys Arg Tyr
 325 330 335

<210> 17
 <211> 1074
 <212> DNA
 <213> METHYLOMONAS SP.

<400> 17
 atgacaaaaa tcttagatgt tgtaaaaccc ggcgttggtca ccggtgaaga tgtgcaaaaa 60
 attttcgcaa tctgcaaaga aaacaacttt gccttgccag ccgtcaacgt gatcagtacc 120
 gataccatta atgcggtatt ggaagcggcc gccaaagcca aatcacctgt tggtatccag 180
 ttttcaaatg gcggcgcgcc tttcgttgcc ggtaaagggt tgaaattgga aggtcaaggc 240
 tgttcgattc atggtgccat ttcaggtgct caccacgttc accgcttggc ggaactctat 300
 ggtgtacctg tcgttctgca taccgaccac gcggcgaaaa aattgctgcc atgggtagat 360
 ggtatgctgg atgaagggtga aaaattcttt gcggccaccg gcaagccttt gttcagctcg 420
 cacatgctgg acttgctcga agagagcctg gaagaaaaca tcgaaatctg cggtaaatac 480
 ttggcgcgca tggcgaaaat gggatatgacc ttggaaatcg aactgggctg caccggcggt 540
 gaagaagacg gcgtggacaa cagcggcatg gatcattccg cgttggtacac ccagccggaa 600
 gacgtggctt acgcgtatga gcacctgagc aaaatcagcc ctaacttcac gattgctggc 660
 tctttcggca acgtgcacgg cgtttactcg ccaggaaacg tcaagctgac gccaaaaatt 720
 ctggataact cgcaaaaata cgtatccgaa aaattcggct tgccagctaa atcattgacc 780
 ttcgtattcc atggcggtc tggttcgtct ccggaagaaa tcaaggaatc catcagctat 840
 ggcgtagtga aaatgaacat cgataccgat acccaatggg caacctggga aggcgtgatg 900
 aacttctaca agaaaaacga aggtatctg caaggccaga tcggcaatcc ggaagggtgcc 960
 gacaagccga acaaaaaata ctatgaccca cgcgtatggc aacgtgccgg ccaagaaggc 1020
 atggttgacac gtctgcaaca agcattccag gaattgaatg cagtaaacac gctg 1074

<210> 18
 <211> 358
 <212> PRT
 <213> METHYLOMONAS SP.

<400> 18
 Met Thr Lys Ile Leu Asp Val Val Lys Pro Gly Val Val Thr Gly Glu
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 Asp Val Gln Lys Ile Phe Ala Ile Cys Lys Glu Asn Asn Phe Ala Leu
 20 25 30
 Pro Ala Val Asn Val Ile Ser Thr Asp Thr Ile Asn Ala Val Leu Glu
 35 40 45
 Ala Ala Ala Lys Ala Lys Ser Pro Val Val Ile Gln Phe Ser Asn Gly
 50 55 60

Gly	Ala	Ala	Phe	Val	Ala	Gly	Lys	Gly	Leu	Lys	Leu	Glu	Gly	Gln	Gly	
65					70					75					80	
Cys	Ser	Ile	His	Gly	Ala	Ile	Ser	Gly	Ala	His	His	Val	His	Arg	Leu	
				85					90					95		
Ala	Glu	Leu	Tyr	Gly	Val	Pro	Val	Val	Leu	His	Thr	Asp	His	Ala	Ala	
			100					105					110			
Lys	Lys	Leu	Leu	Pro	Trp	Val	Asp	Gly	Met	Leu	Asp	Glu	Gly	Glu	Lys	
		115					120					125				
Phe	Phe	Ala	Ala	Thr	Gly	Lys	Pro	Leu	Phe	Ser	Ser	His	Met	Leu	Asp	
	130					135					140					
Leu	Ser	Glu	Glu	Ser	Leu	Glu	Glu	Asn	Ile	Glu	Ile	Cys	Gly	Lys	Tyr	
145					150					155					160	
Leu	Ala	Arg	Met	ala	Lys	Met	Gly	Met	Thr	Leu	Glu	Ile	Glu	Leu	Gly	
			165						170						175	
Cys	Thr	Gly	Gly	Glu	Glu	Asp	Gly	Val	Asp	Asn	Ser	Gly	Met	Asp	His	
		180						185					190			
Ser	Ala	Leu	Tyr	Thr	Gln	Pro	Glu	Asp	Val	Ala	Tyr	Ala	Tyr	Glu	His	
		195					200					205				
Leu	Ser	Lys	Ile	Ser	Pro	Asn	Phe	Thr	Ile	Ala	Ala	Ser	Phe	Gly	Asn	
	210					215					220					
Val	His	Gly	Val	Tyr	Ser	Pro	Gly	Asn	Val	Lys	Leu	Thr	Pro	Lys	Ile	
225					230					235					240	
Leu	Asp	Asn	Ser	Gln	Lys	Tyr	Val	Ser	Glu	Lys	Phe	Gly	Leu	Pro	Ala	
				245					250					255		
Lys	Ser	Leu	Thr	Phe	Val	Phe	His	Gly	Gly	Ser	Gly	Ser	Ser	Pro	Glu	
			260					265					270			
Glu	Ile	Lys	Glu	Ser	Ile	Ser	Tyr	Gly	Val	Val	Lys	Met	Asn	Ile	Asp	
		275					280					285				
Thr	Asp	Thr	Gln	Trp	Ala	Thr	Trp	Glu	Gly	Val	Met	Asn	Phe	Tyr	Lys	
	290					295					300					
Lys	Asn	Glu	Gly	Tyr	Leu	Gln	Gly	Gln	Ile	Gly	Asn	Pro	Glu	Gly	Ala	
305					310					315					320	
Asp	Lys	Pro	Asn	Lys	Lys	Tyr	Tyr	Asp	Pro	Arg	Val	Trp	Gln	Arg	Ala	
				325					330					335		
Gly	Gln	Glu	Gly	Met	Val	Ala	Arg	Leu	Gln	Gln	Ala	Phe	Gln	Glu	Leu	
			340					345					350			
Asn	Ala	Val	Asn	Thr	Leu											
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<210> 19
<211> 636

<212> DNA

<213> METHYLOMONAS SP.

<400> 19

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ttgaaagttt tggagatcac attgcgcacg ccggtggcac tggaaatgat ccgacgtatc 180
aaagccgaag taccggacgc catcgtcggc gcgggcacca tcatcaaccc tcataccttg 240
tatcaagcga ttgacgccgg tgcggaattc atcgtcagcc ccggcatcac cgaaaatcta 300
ctcaacgaag cgctagcatc cggcgtgcct atcctgcccg gcgtcatcac acccagcgag 360
gtcatgcgtt tattgaaaaa aggcattcaat gcgatgaaat tctttccggc tgaagccgcc 420
ggcggcatac cgatgctgaa atcccttggc ggccccttgc cgcaagtcac cttctgtccg 480
accggcggcg tcaatcccaa aaacgcgccc gaatatctgg cattgaaaaa tgtcgcctgc 540
gtcggcgggt cctggatggc gccggccgat ctggtagatg ccgaagactg ggcggaaatc 600
acgcggcggg cgagcgaggg cgcggcattg aaaaaa 636
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<210> 20

<211> 212

<212> PRT

<213> METHYLOMONAS SP.

<400> 20

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Glu Asn Thr Met Ser Val Thr Ile Lys Glu Val Met Thr Thr Ser Pro
 1              5              10              15

Val Met Pro Val Met Val Ile Asn His Leu Glu His Ala Val Pro Leu
      20              25              30

Ala Arg Ala Leu Val Asp Gly Gly Leu Lys Val Leu Glu Ile Thr Leu
      35              40              45

Arg Thr Pro Val Ala Leu Glu Cys Ile Arg Arg Ile Lys Ala Glu Val
      50              55              60

Pro Asp Ala Ile Val Gly Ala Gly Thr Ile Ile Asn Pro His Thr Leu
      65              70              75              80

Tyr Gln Ala Ile Asp Ala Gly Ala Glu Phe Ile Val Ser Pro Gly Ile
      85              90              95

Thr Glu Asn Leu Leu Asn Glu Ala Leu Ala Ser Gly Val Pro Ile Leu
      100              105              110

Pro Gly Val Ile Thr Pro Ser Glu Val Met Arg Leu Leu Glu Lys Gly
      115              120              125

Ile Asn Ala Met Lys Phe Phe Pro Ala Glu Ala Ala Gly Gly Ile Pro
      130              135              140

Met Leu Lys Ser Leu Gly Gly Pro Leu Pro Gln Val Thr Phe Cys Pro
      145              150              155              160

Thr Gly Gly Val Asn Pro Lys Asn Ala Pro Glu Tyr Leu Ala Leu Lys
      165              170              175

Asn Val Ala Cys Val Gly Gly Ser Trp Met ala Pro Ala Asp Leu Val
      180              185              190
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Asp Ala Glu Asp Trp Ala Glu Ile Thr Arg Arg Ala Ser Glu Ala Ala
 195 200 205

Ala Leu Lys Lys
 210

<210> 21
 <211> 873
 <212> DNA
 <213> Methylobionas 16a

<400> 21
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 accaaggccg ttgccaaagga aatgttgccg gtggtggaca agccgctgat tcagtatgcg 120
 gtggaagagg ccgtggccgc cggcatcgac acgatgattt tcgtgatcgg tagaaacaag 180
 gaatccattg ccaaccattt cgataaatcc tacgaactgg aaaaggaact ggaaaaaagc 240
 ggcaagaccg atttgctgaa aatgctgcgg gagattttgc ccgcgcgatgt gtcctgcgta 300
 ttcgtgcgtc aagcggaggc tctgggtttg gggcatgcgg tgcattgcgc caagccggtg 360
 gtcggcaacg agccgtttgc ggtgatcttg ccggatgact tgatcgagga cggcgagcgc 420
 ggttgcatga agcagatggt ggatttggtc gacaaagagc aaagcagcgt attgggggta 480
 gagcgggtcg atcccaagga aaccataag tacggcatcg tcgaacatgc cgaaacctcg 540
 cccagagtcg gttgggttgag ttccatcgtc gagaaacca aaccgaagt ggcgccctcc 600
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 acggggcgcg gcgccggcg cgaaattcaa ttgaccgatg cgattgccgc gttgatgaaa 720
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 <212> PRT
 <213> Methylobionas 16a

<400> 22
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 Ala Gly Ile Asp Thr Met Ile Phe Val Ile Gly Arg Asn Lys Glu Ser
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 Ile Ala Asn His Phe Asp Lys Ser Tyr Glu Leu Glu Lys Glu Leu Glu
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 Lys Ser Gly Lys Thr Asp Leu Leu Lys Met Leu Arg Glu Ile Leu Pro
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 Ala His Val Ser Cys Val Phe Val Arg Gln Ala Glu Ala Leu Gly Leu
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 Gly His Ala Val His Cys Ala Lys Pro Val Val Gly Asn Glu Pro Phe
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Ala Val Ile Leu Pro Asp Asp Leu Ile Glu Asp Gly Glu Arg Gly Cys
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Met Lys Gln Met Val Asp Leu Phe Asp Lys Glu Gln Ser Ser Val Leu
145 150 155 160

Gly Val Glu Arg Val Asp Pro Lys Glu Thr His Lys Tyr Gly Ile Val
165 170 175

Glu His Ala Glu Thr Ser Pro Arg Val Gly Trp Leu Ser Ser Ile Val
180 185 190

Glu Lys Pro Lys Pro Glu Val Ala Pro Ser Asn Ile Ala Val Val Gly
195 200 205

Arg Tyr Ile Leu Thr Pro Ala Ile Phe Gln Lys Ile Glu Asn Thr Gly
210 215 220

Arg Gly Ala Gly Gly Glu Ile Gln Leu Thr Asp Ala Ile Ala Ala Leu
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Met Lys Asp Glu Arg Val Leu Ser Tyr Glu Phe Glu Gly Asn Arg Tyr
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Asp Cys Gly Ser Lys Phe Gly Phe Leu Leu Ala Asn Val Glu Tyr Gly
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Arg Val Ser Lys Ile
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<210> 23

<211> 1419

<212> DNA

<213> Methylomonas 16a

<400> 23

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<210> 24

<211> 473

<212> PRT

<213> Methylomonas 16a

<400> 24

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Gly	His	Thr	Val	Ile	Leu	Leu	Leu	Arg	Val	Ile	Asp	Val	Val	Met	Leu	20	25	30	
Leu	Gly	Ala	Ala	Trp	Leu	Ala	His	Tyr	Phe	Trp	Leu	His	Asp	Ser	Val	35	40	45	
Ile	Asp	Gln	His	Tyr	Arg	Phe	Val	Ile	Ala	Leu	Gly	Ile	Leu	Gly	Ala	50	55	60	
Ile	Ile	Phe	Phe	Glu	Ile	Gly	Gln	Val	Tyr	Arg	Pro	Trp	Arg	Asn	Asp	65	70	75	80
Ala	Met	Arg	Gly	Glu	Ile	Pro	Arg	Ile	Ile	Arg	Ala	Trp	Leu	Leu	Ala	85	90	95	
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Phe	Gly	Ser	Ser	Tyr	Arg	Trp	Ile	Ala	Ser	Trp	Gly	Gly	Leu	Gly	Leu	115	120	125	
Phe	Phe	Val	Leu	Ala	Ala	Arg	Gly	Val	Leu	Ala	Gln	Val	Leu	Lys	Trp	130	135	140	
Leu	Arg	Ala	Arg	Gly	Trp	Ser	Gln	Gly	Arg	Ile	Ile	Leu	Val	Gly	Leu	145	150	155	160
Asn	Gln	Met	ala	Val	Ala	Val	Ser	Arg	Gln	Leu	Asn	His	Ser	Ser	Trp	165	170	175	
Ala	Gly	Leu	Gln	Val	Ile	Gly	Tyr	Val	Asp	Asp	Arg	Ala	Glu	Asp	Arg	180	185	190	
Leu	Ala	Val	Ala	Asp	Tyr	Ser	Leu	Pro	Arg	Leu	Gly	Lys	Leu	Ser	Asp	195	200	205	
Leu	Pro	Arg	Leu	Val	Ser	Arg	Gln	Ala	Val	Asp	Glu	Val	Trp	Val	Ala	210	215	220	
Phe	Pro	Gly	Ala	Ser	Leu	Ala	Glu	Arg	Val	Gln	His	Glu	Leu	Arg	His	225	230	235	240
Leu	Pro	Val	Ser	Ile	Arg	Leu	Val	Ile	Asp	Cys	Phe	Ala	Phe	Lys	Gln	245	250	255	

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 Val Ser Val Ser Pro Leu His Gly Val Asn Arg Tyr Ile Lys Glu Ile
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 Phe Tyr Lys Gln Val Arg Val Gly Trp Asn Asn Arg Lys Phe Thr Met
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 Val Trp Ala Arg Pro Gly Glu Asn Arg Ala Thr Arg Phe Gly Ala Phe
 355 360 365
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 Lys Gly Asp Met Ser Leu Val Gly Pro Arg Pro Glu Arg Pro Asp Phe
 385 390 395 400
 Val Glu Val Phe Lys Asp Gln Val Pro Asn Tyr Met Lys Lys His Met
 405 410 415
 Val Lys Ala Gly Ile Thr Gly Trp Ala Gln Val Asn Gly Trp Arg Gly
 420 425 430
 Asp Thr Asp Leu Asn Arg Arg Ile Glu His Asp Leu Tyr Tyr Ile Gln
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 His Trp Ser Val Trp Phe Asp Leu Glu Ile Ala Phe Arg Thr Val Leu
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 Thr Gly Phe Ile Asn Lys Asn Ala Tyr
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<211> 1098

<212> DNA

<213> Methylomonas 16a

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<210> 26

<211> 366

<212> PRT

<213> Methylobionas 16a

<400> 26

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          20          25          30

Ile Glu Leu Pro Thr Met Lys Gly Gly Gln Leu Val Lys Glu Lys Thr
          35          40          45

Arg Ile Gln Pro Ile Thr Ala Asp Leu Ile Ile Glu Arg Glu Val Ala
          50          55          60

Arg Arg Gln Ala Val Asn Asn Leu Pro Pro Met Asp Glu Thr Arg Thr
          65          70          75          80

Ser Tyr Arg Ile Gly Pro Gln Asp Arg Leu Gln Ile Thr Val Trp Glu
          85          90          95

His Pro Glu Leu Asn Asp Pro Gly Gly Glu Lys Ile Leu Pro Glu Leu
          100          105          110

Ala Gly Lys Val Val Asp Asp Asn Gly Asp Leu Tyr Tyr Pro Tyr Val
          115          120          125

Gly Thr Leu His Val Gly Gly Lys Thr Val Thr Glu Val Arg Glu Glu
          130          135          140

Leu Thr Arg Glu Leu Ser Lys Tyr Phe Lys Lys Val Lys Leu Asp Ile
          145          150          155          160

Arg Val Leu Ser Phe Gln Ala His Arg Val Ala Val Val Gly Glu Val
          165          170          175

Arg Asn Pro Gly Ile Val Ala Met Thr Glu Thr Pro Leu Thr Val Ala
          180          185          190

Glu Ala Ile Ser Arg Ala Gly Gly Ala Thr Gln Asp Ser Asp Leu Asn
          195          200          205

Asn Val Ala Leu Ala Arg Gly Gly Arg Leu Tyr Lys Leu Asp Val Gln
          210          215          220

Ala Leu Tyr Glu Lys Gly Leu Thr Thr Gln Asn Leu Leu Leu Arg Asp
          225          230          235          240

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 Thr Ser Arg Pro Gly Asp Ile Tyr Val Leu Arg Ala Gly Asp Met Gln
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 Pro Glu Ile Phe Gln Leu Asp Ala Glu Ser Pro Asp Ala Met Ile Leu
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 Ala Glu Gln Phe Pro Leu Gln Pro His Asp Thr Leu Phe Val Gly Thr
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<210> 27

<211> 2337

<212> DNA

<213> Methylobionas 16a

<400> 27

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<210> 28

<211> 779

<212> PRT

<213> *Methylomonas* 16a

<400> 28

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Thr Leu Ala Ile Val Leu Ser Val Thr Met Ile Tyr Leu Val Leu Ala
      35              40              45

Pro Arg Thr Tyr Lys Ala Asp Ala Leu Leu Arg Ile Asp Lys Asn Lys
      50              55              60

Ala Leu Leu Ala Ala Asn Leu Arg Ser Glu Gly Asn Gly Thr Pro Thr
      65              70              75              80

Glu Ala Glu Asn Pro Arg Ala Gln Arg Glu Val Glu Ile Leu Arg Ser
      85              90              95

Arg Ser Val Leu Gly Lys Val Val Glu Asp Leu Asn Leu Val Val Glu
      100             105             110

Ala Ser Pro Arg Tyr Phe Pro Ile Ile Gly Glu Thr Leu Ala Arg Lys
      115             120             125

His Asp Lys His Glu Gly Val Ala Gly Ala Trp Trp Gly Phe Ser Arg
      130             135             140

Trp Ala Trp Gly Gly Glu Lys Leu Lys Ile Glu Arg Phe Glu Val Pro
      145             150             155             160

Asp Arg Tyr Leu Asp Lys Ala Phe Thr Leu Val Ala Leu Glu Ala Gly
      165             170             175

Arg Phe Gln Leu Leu Ser Pro Lys Gly Glu Val Leu Ala Glu Gly Leu
      180             185             190

Leu Gly Glu Thr Leu Thr Ala Asp Ile Gly Glu Ala Ser Pro Val Val
      195             200             205

Val Asn Val Ala Asp Leu Gln Ala His Tyr Gly Thr Glu Phe Glu Leu
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Lys	Gly	Arg	Asp	Pro	Glu	Gln	Leu	Ala	Lys	Ser	Val	Asn	Asp	Ile	Ala	260	265	270	
Ser	Ile	Tyr	Val	Asn	Ala	Thr	Val	Asn	Trp	Glu	Ser	Ala	Glu	Ala	Ser	275	280	285	
Gln	Lys	Leu	Asn	Phe	Leu	Glu	Ser	Gln	Leu	Pro	Leu	Val	Lys	Glu	Asn	290	295	300	
Leu	Glu	Lys	Ala	Glu	Gln	Ala	Leu	Ser	Ala	Tyr	Arg	Gln	Gln	His	Gly	305	310	315	320
Ala	Val	Asp	Ile	Ser	Ala	Glu	Ala	Glu	Ile	Leu	Leu	Lys	Gln	Ala	Ser	325	330	335	
Glu	Met	Glu	Thr	Leu	Ser	Ile	Gln	Leu	Lys	Gln	Lys	Tyr	Asp	Glu	Gln	340	345	350	
Ser	Gln	Arg	Leu	Glu	Ser	Glu	His	Pro	Asp	Met	Ile	Ala	Thr	Asn	Ala	355	360	365	
Gln	Ile	Arg	Arg	Val	Ser	Asn	Lys	Leu	Ala	Ala	Leu	Glu	Lys	Arg	Ile	370	375	380	
Lys	Asp	Leu	Pro	Lys	Thr	Gln	Gln	Asn	Met	Val	Ser	Leu	Ser	Arg	Asp	385	390	395	400
Val	Gln	Val	Asn	Thr	Glu	Leu	Tyr	Thr	Ser	Leu	Leu	Asn	Ser	Ala	Gln	405	410	415	
Glu	Gln	Arg	Ile	Ala	Ala	Ala	Gly	Ser	Leu	Gly	Asn	Ser	Arg	Ile	Val	420	425	430	
Asp	Phe	Ala	Val	Val	Pro	Glu	Lys	Pro	Tyr	Trp	Pro	Lys	Pro	Gly	Leu	435	440	445	
Leu	Leu	Ala	Ile	Ala	Gly	Leu	Leu	Gly	Ile	Ser	Leu	Gly	Ser	Ala	Leu	450	455	460	
Ile	Phe	Leu	Arg	His	Ser	Leu	Gln	Arg	His	Asp	Asn	Tyr	Pro	Ala	Leu	465	470	475	480
Leu	Glu	Tyr	Gln	Val	Gly	Leu	Pro	Leu	Phe	Ala	Ala	Ile	Pro	His	Ser	485	490	495	
Lys	Lys	Gln	Arg	Arg	Leu	Ala	Arg	Leu	Leu	Asp	Gln	Gly	Lys	Glu	Arg	500	505	510	
Asp	Thr	Ala	Ile	Leu	Val	Ser	His	Asp	Pro	Leu	Asp	Ile	Ser	Val	Glu	515	520	525	
Ser	Leu	Arg	Gly	Leu	Arg	Thr	Thr	Leu	Glu	Ala	Thr	Leu	Ala	Ser	Asp	530	535	540	

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 580 585 590
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 Lys Val Ser Leu Gly Asp Val Ile Val Ser Leu Pro Glu Ile Gly Val
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 725 730 735
 Met Arg Gln Lys Gln Thr Thr Ala Trp Gln Ala Arg Phe Gln Asn Leu
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<211> 1416

<212> DNA

<213> Methylomonas 16a

<400> 29

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tttcaagcgg tttcccaagg caaaagcaaa gatgcatgtt cgctgctatg gctgtggata 960
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gccgcgggca cggccttgca tgccctgggc accgtgatgt cccagccgct gctggcgaga 1140
aaacgcacgc cgatcttgct gcgcgggcgt atctgtgggg cgttggcggc gctcatcacg 1200
ctgcctttgc tgggtggcgca ttttggcctg ttcggggcgg ccttggccaa tcccgtatat 1260
ttcggcatcg aagcgtggt gttggccttg ctggccaagc cctggcgcaa gctccgcacg 1320
ggacggcagg cgcggatcgt tcaatccgaa gcggcgatgc ccgaaccgca ctttgacgcc 1380
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<210> 30

<211> 472

<212> PRT

<213> Methylobionas 16a

<400> 30

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Met Leu Gly Lys Gly His Ser Asp Lys Ala Asn Leu Lys Glu Gly Phe
  1              5              10              15

```

```

Met Leu Asp Trp Leu Arg Gln Lys Asn Leu Leu Gly Asp Ala Cys Trp
      20              25              30

```

```

Ala Leu Ala Gly Gln Leu Leu Ser Ala Leu Ala Leu Leu Ala Gly Thr
      35              40              45

```

```

Arg Ile Leu Thr Glu Leu Val Thr Pro Ala Val Phe Gly His Val Ala
      50              55              60

```

```

Leu Leu Asn Gly Phe Val Ala Leu Gly Val Ala Val Phe Ala Tyr Pro
      65              70              75              80

```

```

Phe Ile Cys Ala Gly Met Arg Phe Thr Asn Glu Cys Arg Asn Phe Arg
      85              90              95

```

```

Glu Arg Ala Ala Leu His Gly Leu Val Phe Ala Leu Thr Thr Arg Ser
      100              105              110

```

```

Thr Ala Leu Ala Ile Thr Leu Leu Leu Leu Gly Gly Ala Leu Tyr Cys
      115              120              125

```

```

Tyr Phe Val Gly Ser Glu Ile Gly Leu Phe Val Leu Thr Gly Leu Leu
      130              135              140

```

```

Leu Ala Val Thr Val Arg Arg Glu Leu Gly Ile Gln Leu Met Ile Gly
      145              150              155              160

```

```

Glu Arg Lys Gln Arg Gly Ala Ala Leu Trp Gln Thr Ser Asp Ser Ile
      165              170              175

```

```

Leu Arg Pro Val Met ala Ile Trp Leu Val Trp Gly Leu Gly Gln Ser
      180              185              190

```

Pro Glu Ala Val Leu Leu Gly Tyr Val Cys Ala Ser Val Leu Ala Asn
 195 200 205
 Thr Leu Trp Thr Ile Val Ser Asp Ala Trp Gln Lys Lys Pro Thr Gly
 210 215 220
 Asp Arg Gly Phe Leu Gly Arg Gln Phe Glu Arg Gly Leu Trp Ala Tyr
 225 230 235 240
 Ala Leu Pro Leu Ile Pro Met Glu Leu Met Phe Trp Leu Asn Gly Leu
 245 250 255
 Gly Asp Arg Tyr Val Ile Gly Tyr Phe Leu Thr Ala Ala Glu Val Gly
 260 265 270
 Val Tyr Ala Ala Ala Tyr Thr Leu Val Asn Glu Ala Phe Asn Arg Ser
 275 280 285
 Ala Met Val Leu Leu Arg Thr Phe Gln Pro Ala Tyr Phe Gln Ala Val
 290 295 300
 Ser Gln Gly Lys Ser Lys Asp Ala Cys Ser Leu Leu Trp Leu Trp Ile
 305 310 315 320
 Gly Ala Val Val Val Met Ser Val Leu Gly Val Thr Leu Val Trp Leu
 325 330 335
 Cys Lys Asp Trp Leu Val Ala Gly Leu Leu Ala Glu Pro Tyr His Ala
 340 345 350
 Ala Gly Ala Leu Met Pro Val Ile Ala Ala Gly Thr Ala Leu His Ala
 355 360 365
 Leu Gly Thr Val Met Ser Gln Pro Leu Leu Ala Arg Lys Arg Thr Pro
 370 375 380
 Ile Leu Leu Arg Gly Arg Ile Cys Gly Ala Leu Ala Ala Leu Ile Thr
 385 390 395 400
 Leu Pro Leu Leu Val Ala His Phe Gly Leu Phe Gly Ala Ala Leu Ala
 405 410 415
 Asn Pro Val Tyr Phe Gly Ile Glu Ala Leu Val Leu Ala Leu Leu Ala
 420 425 430
 Lys Pro Trp Arg Lys Leu Arg Thr Gly Arg Gln Ala Arg Ile Val Gln
 435 440 445
 Ser Glu Ala Ala Met Pro Glu Pro Asp Phe Asp Ala Ile Gly Val Arg
 450 455 460
 Ala Ala Ala Phe Ser Asn Glu Ser
 465 470

<210> 31
 <211> 816
 <212> DNA
 <213> Methylobionas 16a

<400> 31
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 gattccggga gcagcgatga cacgctgtcg atcgcggaag gccacggctg caagatttat 180
 caaaatcctt ggccccggtt tgccgagcag cgcaattttg cgttgaatca atgcgatatc 240
 gagacgccgt ggggtgttgtt cgtcgatgcc gacgaaatct acccgcaagt cttttatcag 300
 catttcgaca gtggaatgct gcaaaccgga gagatcgatg tgctgatggt gccgtccatt 360
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 atggatagtt gccgcacgg ctacaccgat attccctatg atcattactt ttacgacggc 540
 gagatcatcc agtggatgca taagcatgct gacaaagccg ctcaggaagt tcggctcaaa 600
 ccgaccagg gcgcgttgat gacgaccgc gggcgcttga gcgtaatgct ggggcgttca 660
 tggagccgaa tcctggccag gtttgtttac cactatctgc tgccggcgcg ctttttggac 720
 ggcgcggcgg gattggaatt tacgctgatg tttacctggt atgaagccag catctatctg 780
 caagccaaag ccgctgcaca agcaagggga acagca 816

<210> 32
 <211> 272
 <212> PRT
 <213> Methylobionas 16a

<400> 32
 Pro Ile Asn Arg Cys Glu Pro Leu Asn Ser Leu Thr Ile Val Ile Leu
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 Thr Leu Asn Glu Ala Ala Asn Leu Pro Arg Cys Leu Ala Ala Ile Pro
 20 25 30
 Gln Arg Tyr Pro Val Val Ile Leu Asp Ser Gly Ser Ser Asp Asp Thr
 35 40 45
 Leu Ser Ile Ala Glu Gly His Gly Cys Lys Ile Tyr Gln Asn Pro Trp
 50 55 60
 Pro Gly Phe Ala Glu Gln Arg Asn Phe Ala Leu Asn Gln Cys Asp Ile
 65 70 75 80
 Glu Thr Pro Trp Val Leu Phe Val Asp Ala Asp Glu Ile Tyr Pro Gln
 85 90 95
 Val Phe Tyr Gln His Phe Asp Ser Gly Met Leu Gln Thr Gly Glu Ile
 100 105 110
 Asp Val Leu Met Val Pro Ser Ile Leu Phe Leu Arg Gly Lys Arg Leu
 115 120 125
 His His Ala Pro Gly Tyr Pro Ile Tyr His Pro Arg Leu Val Arg Arg
 130 135 140
 Glu Thr Thr Arg Phe Val Arg Asn His Thr Gly His Gly Glu Ala Val
 145 150 155 160
 Met Asp Ser Cys Arg Ile Gly Tyr Thr Asp Ile Pro Tyr Asp His Tyr
 165 170 175
 Phe Tyr Asp Gly Glu Ile Ile Gln Trp Met His Lys His Val Asp Lys
 180 185 190

Ala Ala Gln Glu Val Arg Leu Lys Pro Thr Gln Gly Ala Leu Met Thr
195 200 205

Thr Arg Gly Arg Leu Ser Val Met Leu Gly Arg Ser Trp Ser Arg Ile
210 215 220

Leu Ala Arg Phe Val Tyr His Tyr Leu Leu Arg Gly Gly Phe Leu Asp
225 230 235 240

Gly Ala Ala Gly Leu Glu Phe Thr Leu Met Phe Thr Trp Tyr Glu Ala
245 250 255

Ser Ile Tyr Leu Gln Ala Lys Ala Ala Ala Gln Ala Arg Gly Thr Ala
260 265 270

<210> 33
<211> 852
<212> DNA
<213> Methylobionas 16a

<400> 33
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gacggcaaaa tcgatcggat tgcccgagca tatagccaat gcctcgatct gaaacacgctc 180
aagggtgaatt tcaccggtaa tgcccagacc agggatcatg gcatcgccctt ggcccagggc 240
gacatcatcg cctttccgga cgatgattgc gtgtatgaaa aggatgtgct ggaaaaagtg 300
gtaggcgaat ttgcatgcca gccaacgttg tgcattctgg tagccgggtc ctacgatttt 360
tccgcgaaac acttcagcat aggcgtcaac agccgtaaag cgcgttattt tccccggttg 420
aacatgatgg ggggtggagt caccgagttt tttgcgctgg cgcgtatcga caggcggcag 480
ttttatttgg accacgattt cggcatcggc tccaaatatg ccggggcgga aggcttcgag 540
ttgctgtatc gcctgctgcg cgcggggcggg cgggcgttct acaagccgga tatcaaaatc 600
tatcacgcca acaaggacca ttacacgctg ggtaccgcgc gcatgctgaa atattccacc 660
ggatattggcg cctatatccg caaattcgcc aatcagcatg atccctatat cggtatttac 720
atcctgcgca agatgctgat agccccgact ctgaaaatgc tgctggcctt gttgacgttc 780
aaccgggaa aactcgcta ttcgttttat aacctgggtg gcatatggcg cggatttttt 840
gcctatgggc gc 852

<210> 34
<211> 284
<212> PRT
<213> Methylobionas 16a

<400> 34
Met Lys Val Ser Leu Ile Leu Ala Thr Leu Gly Arg Asp Leu Glu Leu
1 5 10 15

Leu Asp Phe Leu Lys Ser Leu Leu Phe Gln Thr Tyr Lys Asn Phe Glu
20 25 30

Leu Ile Val Ile Asp Gln Asn Gln Asp Gly Lys Ile Asp Arg Ile Ala
35 40 45

Glu Gln Tyr Ser Gln Cys Leu Asp Leu Lys His Val Lys Val Asn Phe
50 55 60

Thr Gly Asn Ala Arg Ala Arg Asp His Gly Ile Ala Leu Ala Gln Gly
65 70 75 80

Asp Ile Ile Ala Phe Pro Asp Asp Asp Cys Val Tyr Glu Lys Asp Val
 85 90 95
 Leu Glu Lys Val Val Gly Glu Phe Ala Cys Gln Pro Thr Leu Ser Ile
 100 105 110
 Leu Val Ala Gly Ser Tyr Asp Phe Ser Ala Lys His Phe Ser Ile Gly
 115 120 125
 Val Asn Ser Arg Lys Ala Arg Tyr Phe Ser Arg Leu Asn Met Met Gly
 130 135 140
 Val Glu Phe Thr Gln Phe Phe Ala Leu Ala Arg Ile Asp Arg Arg Gln
 145 150 155 160
 Phe Tyr Leu Asp His Asp Phe Gly Ile Gly Ser Lys Tyr Ala Gly Ala
 165 170 175
 Glu Gly Phe Glu Leu Leu Tyr Arg Leu Leu Arg Ala Gly Gly Arg Ala
 180 185 190
 Phe Tyr Lys Pro Asp Ile Lys Ile Tyr His Ala Asn Lys Asp His Tyr
 195 200 205
 Thr Leu Gly Thr Ala Arg Met Leu Lys Tyr Ser Thr Gly Ile Gly Ala
 210 215 220
 Tyr Ile Arg Lys Phe Ala Asn Gln His Asp Pro Tyr Ile Gly Tyr Tyr
 225 230 235 240
 Ile Leu Arg Lys Met Leu Ile Ala Pro Thr Leu Lys Met Leu Leu Ala
 245 250 255
 Leu Leu Thr Phe Asn Pro Gly Lys Leu Ala Tyr Ser Phe Tyr Asn Leu
 260 265 270
 Val Gly Ile Trp Arg Gly Phe Phe Ala Tyr Gly Arg
 275 280

<210> 35

<211> 1194

<212> DNA

<213> Methylomonas 16a

<400> 35

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tcgtcggatg	aatccatcga	tgggtgcttg	aaaccggcgg	acgtcaagct	gggcgcaagc	180
gtggatgtcg	atgtgtaccg	ctgttatggc	ttcaggecgt	gggggttcgg	cttgggagcg	240
ataccagcc	tgctgcgcct	gtgctggcaa	gccccgctcg	tgtatatcca	tggcgtcgcc	300
acctggccgt	cgaccttggc	ggcgcttttt	tgtgcctgc	tgcgcaagcc	gttcatggtg	360
gcggtgcatg	gcggcctgat	gcctgagcat	gtggcactga	tcaagcggaa	aaaacggcat	420
aaatgggtgg	attacaaact	gctgactttt	ccgaccttgc	gccgcgcgat	tgccgtgcat	480
tgcaccagtg	ataccgaggt	tgagggcgtg	cgtgacgtac	tgggcgaaaa	cgcgcggtg	540
ttgctggtgc	ccaacggcat	cgacagccgg	ggtgtcgagg	aggcccctta	tccggcaggc	600
gaaggcatgc	aactgtgttt	tttgggtcac	gtgcagcagg	aaaagggcat	caacgctttc	660
atccgggcct	ggctcgaggt	ccggcggccg	ggcgatcgtc	tggctcgtcg	cggccgtagc	720
gtggacgggg	attattttgc	cgagttttgt	tccctggtcg	aacgggcaaa	cggcgcgatc	780
cgctattgcg	gctatctgca	gcgtgacgac	gtgatggcct	tgctggcgca	aagtcatttt	840

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ctggtattgc cgtccggttt ggagcaggtc ggcgccatgc gggagaattt cggtaacgtg 900
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catttgccgg cattgaatgc gggcttggtt tttgacaggg acgaggccgc cgtccaagcc 1020
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cggcgccatg ttcaacagca gctcgatccg gtcaaactgg cggagcgcgt ctggcaagca 1140
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<210> 36

<211> 398

<212> PRT

<213> Methylobionas 16a

<400> 36

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Met Glu Leu Gly Ile Val Thr Thr His Val Pro Pro Ala Lys Gly Tyr
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Gly Gly Val Ser Val Thr Cys Gly Val Leu Thr Arg Ala Trp Ala Glu
          20             25             30

Met Gly Leu Glu Met ala Leu Val Ser Ser Asp Glu Ser Ile Asp Gly
          35             40             45

Cys Leu Lys Pro Ala Asp Val Lys Leu Gly Ala Ser Val Asp Val Asp
          50             55             60

Leu Tyr Arg Cys Tyr Gly Phe Arg Arg Trp Gly Phe Gly Leu Gly Ala
          65             70             75             80

Ile Pro Ser Leu Leu Arg Leu Cys Trp Gln Ala Pro Leu Val Tyr Ile
          85             90             95

His Gly Val Ala Thr Trp Pro Ser Thr Leu Ala Ala Leu Phe Cys Cys
          100             105             110

Leu Leu Arg Lys Pro Phe Met Val Ala Val His Gly Gly Leu Met Pro
          115             120             125

Glu His Val Ala Leu Ile Lys Arg Lys Lys Arg His Lys Trp Trp Tyr
          130             135             140

Tyr Lys Leu Leu Thr Phe Pro Thr Leu Arg Arg Ala Ile Ala Val His
          145             150             155             160

Cys Thr Ser Asp Thr Glu Val Glu Gly Val Arg Asp Val Leu Gly Glu
          165             170             175

Asn Ala Arg Val Leu Leu Val Pro Asn Gly Ile Asp Ser Arg Gly Val
          180             185             190

Glu Glu Ala Pro Tyr Pro Ala Gly Glu Gly Met Gln Leu Cys Phe Leu
          195             200             205

Gly His Val Gln Gln Glu Lys Gly Ile Asn Ala Phe Ile Arg Ala Trp
          210             215             220

Leu Glu Val Arg Arg Pro Gly Asp Arg Leu Val Val Ala Gly Arg Ser
          225             230             235             240

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Val Asp Gly Asp Tyr Phe Ala Glu Phe Cys Ser Leu Val Glu Arg Ala
 245 250 255
 Asn Gly Ala Ile Arg Tyr Cys Gly Tyr Leu Gln Arg Asp Asp Val Met
 260 265 270
 Ala Leu Leu Ala Gln Ser His Phe Leu Val Leu Pro Ser Gly Leu Glu
 275 280 285
 Gln Val Gly Gly Met Arg Glu Asn Phe Gly Asn Val Val Ala Glu Ala
 290 295 300
 Leu Ala Ala Gly Arg Pro Val Leu Val Val Arg Gly Leu Ala Trp Asp
 305 310 315 320
 His Leu Pro Ala Leu Asn Ala Gly Leu Val Phe Asp Arg Asp Glu Ala
 325 330 335
 Ala Val Gln Ala Val Leu Arg Arg Ala Gln Ala Leu Asp Gln Ala Asp
 340 345 350
 Trp Leu Arg Met Ser Gln Ala Gly Arg Arg His Val Gln Gln Gln Leu
 355 360 365
 Asp Pro Val Lys Leu Ala Glu Arg Val Trp Gln Ala Met Thr Ala Ala
 370 375 380
 Val Pro Val Asp Glu Ala Lys Val Leu Ala Glu Glu Pro Lys
 385 390 395

<210> 37

<211> 951

<212> DNA

<213> *Methylomonas* 16a

<400> 37

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tcgtccagcg acgacacggt ggcgctggcc cgtgcgagag gatttgacgc gcatgtgatt 180
gccaaggcct cgttcaacca cggcggcact cgtcaatcgg gcgtcgatat gttggctcgac 240
atggatctga tcgtattttct gacccaggat gccttggttg cgcacccag cgcgatcgaa 300
aatctgttgc aggtattttgt caatccgcaa gtggccgcgg cctatggccg gcaattgccg 360
catcggaacg ctggccccat cggcgcgcat gcccgatat tcaattaccc ggcgcaaagc 420
cagttgcgca ccttgcagga ccgcgaccgc ttcggcatca agaccgtgtt catttccaat 480
tcgttcgccc cctacagacg ttgcgccctg atgcaaateg gcggattccc ggctcacacc 540
attatgaacg aagataactta cgttgccggc aagatgctgt tgtccggctg gagcctcgcc 600
tattgcgcgg acgcgcgggt gtttcattcc cacgattaca gcctgctgga agaattcagg 660
cgctatttcg atacgggggt tttccacgcg caaaaccctt ggctgcaaca gacctttggc 720
ggcgccctcg gcgaaggcgc gcggttttgt ctctccgaaa tgcgttactt gtcgaacacg 780
gcgccttggc tgatgttttc cgcgttcctg agaacgggat tgaaatgggc ggggtataag 840
ctgggcggcc tgcacgcggc ctggccatta gccctgagca ggcgccctcag cctgcataag 900
ggatattggg tggcaactga acgggaatac cctaataatgc ctggatgccg t 951
  
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<210> 38

<211> 317

<212> PRT

<213> *Methylomonas* 16a

<400> 38

Met	Thr	His	Lys	Val	Gly	Leu	Val	Val	Pro	Thr	Leu	Asn	Ala	Gly	Ala	1	5	10	15
Ser	Trp	Gln	Gly	Trp	Leu	Glu	Ala	Leu	Ala	Ala	Gln	Ser	Arg	Arg	Pro	20	25	30	
Asp	Arg	Leu	Leu	Leu	Ile	Asp	Ser	Ser	Ser	Ser	Asp	Asp	Thr	Val	Ala	35	40	45	
Leu	Ala	Arg	Ala	Arg	Gly	Phe	Asp	Ala	His	Val	Ile	Ala	Lys	Ala	Ser	50	55	60	
Phe	Asn	His	Gly	Gly	Thr	Arg	Gln	Ser	Gly	Val	Asp	Met	Leu	Val	Asp	65	70	75	80
Met	Asp	Leu	Ile	Val	Phe	Leu	Thr	Gln	Asp	Ala	Leu	Leu	Ala	Asp	Pro	85	90	95	
Ser	Ala	Ile	Glu	Asn	Leu	Leu	Gln	Val	Phe	Val	Asn	Pro	Gln	Val	Ala	100	105	110	
Ala	Ala	Tyr	Gly	Arg	Gln	Leu	Pro	His	Arg	Asn	Ala	Gly	Pro	Ile	Gly	115	120	125	
Ala	His	Ala	Arg	Ile	Phe	Asn	Tyr	Pro	Ala	Gln	Ser	Gln	Leu	Arg	Thr	130	135	140	
Leu	Gln	Asp	Arg	Asp	Arg	Phe	Gly	Ile	Lys	Thr	Val	Phe	Ile	Ser	Asn	145	150	155	160
Ser	Phe	Ala	Ala	Tyr	Arg	Arg	Cys	Ala	Leu	Met	Gln	Ile	Gly	Gly	Phe	165	170	175	
Pro	Ala	His	Thr	Ile	Met	Asn	Glu	Asp	Thr	Tyr	Val	Ala	Gly	Lys	Met	180	185	190	
Leu	Leu	Ser	Gly	Trp	Ser	Leu	Ala	Tyr	Cys	Ala	Asp	Ala	Arg	Val	Phe	195	200	205	
His	Ser	His	Asp	Tyr	Ser	Leu	Leu	Glu	Glu	Phe	Arg	Arg	Tyr	Phe	Asp	210	215	220	
Ile	Gly	Val	Phe	His	Ala	Gln	Asn	Pro	Trp	Leu	Gln	Gln	Thr	Phe	Gly	225	230	235	240
Gly	Ala	Ser	Gly	Glu	Gly	Ala	Arg	Phe	Val	Leu	Ser	Glu	Met	Arg	Tyr	245	250	255	
Leu	Ser	Asn	Thr	Ala	Pro	Trp	Leu	Met	Phe	Ser	Ala	Phe	Leu	Arg	Thr	260	265	270	
Gly	Leu	Lys	Trp	Ala	Gly	Tyr	Lys	Leu	Gly	Gly	Leu	His	Arg	Gly	Trp	275	280	285	
Pro	Leu	Ala	Leu	Ser	Arg	Arg	Leu	Ser	Leu	His	Lys	Gly	Tyr	Trp	Val	290	295	300	
Ala	Thr	Glu	Arg	Glu	Tyr	Pro	Asn	Met	Pro	Gly	Cys	Arg	305	310	315				

<210> 39
 <211> 1170
 <212> DNA
 <213> *Methylobacterium* 16a

<220>
 <223> ORF1

<220>
 <223> nirF gene

<400> 39
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 gacctgcgcg ccaccggcga tttgggtgtc gtgatcgagc ggcagaccgg cagtgtgcaa 120
 gtcatacaaca ccagcacgcc caagatgctg agccgcacgc aaggcctggg cgatttgtct 180
 cagcgttcgg tgggtgttct gcgtgatcag cgctatgcct atgtattcgg tcgcgacggc 240
 ggcttgagca aaatcgatct gttgcaggac aaaatcgaaa aacgcgtcgt gcaagccggt 300
 aacagcatag gcggggcgat ttcccaggat ggcaaagtca tcgccgtatc caactatacg 360
 ccggggcgcg tcaagctgtt cgatgccgag accttgagc agttggccga gattccggcc 420
 gtttacggcg acgacaacca gttatccaaa gtggtcggct tggtcgatgc accggggcgg 480
 cgtttcgttt gcagcctgtt cgaaggtaac gagatttggc tgatagacgc caagaatcca 540
 cgccagccgg tcgtcaagaa attcaaggac atcggcaagc ggccttatga tgccttgctg 600
 acgccggatg gccatttcta cgcgcccgga ctgttcggcg aaaaaggcct ggctttgctg 660
 gatttatggc agccggagct aggcgtcaaa cacatcctgg aagactacgg caaggacgac 720
 gagcaattgc cgggtttacaa aatgccgcat ctggaaggct ggacggtagc cggatgatcg 780
 ctgttcgtgc cggccatcgg cctgcatgag gtgttggtga tcgataaaca cgattgggag 840
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 aaggatttca atatcgtcaa gaccctgcaa ccgggtaagg ccgtgctgca catggagtgc 1020
 agcccgcgcg gcgaagccgt ctggatggcg gtgcgcgacg aggacagggt aatgggttac 1080
 gacacggaca gtttcaacga aaccgcccgt ctaccggcgc aaaagcccag cggcatcttt 1140
 ttcagtaatc gcgccaatca gttggggctg 1170

<210> 40
 <211> 390
 <212> PRT
 <213> *Methylobacterium* 16a

<220>
 <223> NirF

<400> 40
 Met Lys Arg Phe Leu Thr Leu Ala Gly Ala Ala Tyr Phe Phe Ala Ala
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 Ser Ala Val Ala Asp Leu Arg Ala Thr Gly Asp Leu Gly Val Val Ile
 20 25 30
 Glu Arg Glu Thr Gly Ser Val Gln Val Ile Asn Thr Ser Thr Pro Lys
 35 40 45
 Met Leu Ser Arg Ile Glu Gly Leu Gly Asp Leu Ser His Ala Ser Val
 50 55 60
 Val Phe Ser Arg Asp Gln Arg Tyr Ala Tyr Val Phe Gly Arg Asp Gly
 65 70 75 80
 Gly Leu Ser Lys Ile Asp Leu Leu Gln Asp Lys Ile Glu Lys Arg Val
 85 90 95

Val	Gln	Ala	Gly	Asn	Ser	Ile	Gly	Gly	Ala	Ile	Ser	Gln	Asp	Gly	Lys	100	105	110
Val	Ile	Ala	Val	Ser	Asn	Tyr	Thr	Pro	Gly	Gly	Val	Lys	Leu	Phe	Asp	115	120	125
Ala	Glu	Thr	Leu	Glu	Gln	Leu	Ala	Glu	Ile	Pro	Ala	Val	Tyr	Gly	Asp	130	135	140
Asp	Asn	Gln	Leu	Ser	Lys	Val	Val	Gly	Leu	Val	Asp	Ala	Pro	Gly	Gly	145	150	155
Arg	Phe	Val	Cys	Ser	Leu	Phe	Glu	Gly	Asn	Glu	Ile	Trp	Leu	Ile	Asp	165	170	175
Ala	Lys	Asn	Pro	Arg	Gln	Pro	Val	Val	Lys	Lys	Phe	Lys	Asp	Ile	Gly	180	185	190
Lys	Arg	Pro	Tyr	Asp	Ala	Leu	Leu	Thr	Pro	Asp	Gly	His	Phe	Tyr	Ala	195	200	205
Ala	Gly	Leu	Phe	Gly	Glu	Lys	Gly	Leu	Ala	Leu	Leu	Asp	Leu	Trp	Gln	210	215	220
Pro	Glu	Leu	Gly	Val	Lys	His	Ile	Leu	Glu	Asp	Tyr	Gly	Lys	Asp	Asp	225	230	235
Glu	Gln	Leu	Pro	Val	Tyr	Lys	Met	Pro	His	Leu	Glu	Gly	Trp	Thr	Val	245	250	255
Ala	Gly	Asp	Leu	Leu	Phe	Val	Pro	Ala	Ile	Gly	Leu	His	Glu	Val	Leu	260	265	270
Val	Ile	Asp	Lys	His	Asp	Trp	Glu	Leu	Val	Lys	Arg	Ile	Pro	Val	Val	275	280	285
Gly	Gln	Pro	Val	Phe	Val	Met	Ser	Arg	Pro	Asp	Gly	Arg	Gln	Val	Trp	290	295	300
Val	Asn	Phe	Ala	Phe	Pro	Asp	Asn	Gln	Thr	Val	Gln	Val	Ile	Asp	Val	305	310	315
Lys	Asp	Phe	Asn	Ile	Val	Lys	Thr	Leu	Gln	Pro	Gly	Lys	Ala	Val	Leu	325	330	335
His	Met	Glu	Phe	Ser	Pro	Arg	Gly	Glu	Ala	Val	Trp	Met	ala	Val	Arg	340	345	350
Asp	Glu	Asp	Arg	Val	Met	Val	Tyr	Asp	Thr	Asp	Ser	Phe	Asn	Glu	Thr	355	360	365
Ala	Arg	Leu	Pro	Ala	Gln	Lys	Pro	Ser	Gly	Ile	Phe	Phe	Ser	Asn	Arg	370	375	380
Ala	Asn	Gln	Leu	Gly	Leu											385	390	

<210> 41
<211> 453

<212> DNA
 <213> *Methylobacterium* 16a

<220>
 <223> ORF2

<220>
 <223> nirD gene

<400> 41
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 ccgacaccgt ttctggatat cgccgagcag cttggcgctc cggaaggcga agtgctggcg 120
 gcgttttcagg tgttgccga gcagcaaatg atcagccgca tcggccccgt gatcgcgccg 180
 aacgccatcg gcaatagcgc cttggtggcg atggcggtgc cggagcagga tttggccccgt 240
 gtcgcccgcct tggtagcgc ctatccggaa gtcaatcata actatgagcg ggaaaaccgc 300
 ttcaatttgt ggtttggtgt gatcgccctc gatcatactc acttgacgagc ggtgattgcc 360
 gatatcgaga ctcaaaccgg ttatcaagcc atgctgttgc cgatgctggc cgattatttc 420
 atcaacctgg gttttgaact caatctgaac gac 453

<210> 42
 <211> 151
 <212> PRT
 <213> *Methylobacterium* 16a

<220>
 <223> NirD

<400> 42
 Met Leu Ala Ser Leu His Lys His Leu Leu Asn Asp Tyr Gln Gln Asp
 1 5 10 15
 Phe Pro Leu Ser Pro Thr Pro Phe Leu Asp Ile Ala Glu Gln Leu Gly
 20 25 30
 Val Thr Glu Gly Glu Val Leu Ala Ala Phe Gln Val Leu Ala Glu Gln
 35 40 45
 Gln Met Ile Ser Arg Ile Gly Pro Val Ile Ala Pro Asn Ala Ile Gly
 50 55 60
 Asn Ser Ala Leu Val Ala Met ala Val Pro Glu Gln Asp Leu Ala Arg
 65 70 75 80
 Val Ala Ala Leu Val Ser Ala Tyr Pro Glu Val Asn His Asn Tyr Glu
 85 90 95
 Arg Glu Asn Arg Phe Asn Leu Trp Phe Val Leu Ile Ala Ser Asp His
 100 105 110
 Thr His Leu Gln Arg Val Ile Ala Asp Ile Glu Thr Gln Thr Gly Tyr
 115 120 125
 Gln Ala Met Leu Leu Pro Met Leu Ala Asp Tyr Phe Ile Asn Leu Gly
 130 135 140
 Phe Glu Leu Asn Leu Asn Asp
 145 150

<210> 43
 <211> 504

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<212> DNA
<213> Methylobacterium 16a

<220>
<223> ORF3

<220>
<223> nirL gene

<400> 43
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cggccctatg ccgccatcgc cgcgaaattg gacatggacg aacaggacgt catcgcccga 120
ctgggacgct tgaaaacgga aggtttgatc aggcgctggg gcgtcgtggt caagcaccgg 180
caactagggt atcgcgccaa tgcgatgatc gtgatggata ttctgatga tcaagttgcg 240
gaaatggggc ggcgtgtcag ccagcacagc ttcgtcaatc tgtgttatcg ccgaccacgt 300
caaggcgagg tttggccgta taacctttat tgcgatgata acggcaaaaa tcgcgagacg 360
gttttgcagc aatggggccga tctgcaacaa agttgcggcc tggaagcctg tcggcagcag 420
atattattca gtcgtcgttg tttcaagcag cgtgggggcta tttataaagc gcccggtgatt 480
gagccattgg agtttagtca tgga 504

<210> 44
<211> 168
<212> PRT
<213> Methylobacterium 16a

<220>
<223> NirL

<400> 44
Met Asp Ala Leu Asp Tyr Arg Leu Ile Ala Ala Val Gln Ala Gly Leu
 1 5 10 15

Pro Leu Thr Ala Arg Pro Tyr Ala Ala Ile Ala Ala Lys Leu Asp Met
 20 25 30

Asp Glu Gln Asp Val Ile Ala Arg Leu Gly Arg Leu Lys Thr Glu Gly
 35 40 45

Leu Ile Arg Arg Trp Gly Val Val Val Lys His Arg Gln Leu Gly Tyr
 50 55 60

Arg Ala Asn Ala Met Ile Val Met Asp Ile Pro Asp Asp Gln Val Ala
 65 70 75 80

Glu Met Gly Arg Arg Val Ser Gln His Ser Phe Val Asn Leu Cys Tyr
 85 90 95

Arg Arg Pro Arg Gln Gly Glu Val Trp Pro Tyr Asn Leu Tyr Cys Met
 100 105 110

Ile His Gly Lys Asn Arg Glu Thr Val Leu Gln Gln Trp Ala Asp Leu
 115 120 125

Gln Gln Ser Cys Gly Leu Glu Ala Cys Arg His Glu Ile Leu Phe Ser
 130 135 140

Arg Arg Cys Phe Lys Gln Arg Gly Ala Ile Tyr Lys Ala Pro Val Ile
 145 150 155 160

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Glu Pro Leu Glu Phe Ser His Gly
165

<210> 45
<211> 441
<212> DNA
<213> *Methylobacterium* 16a

<220>
<223> ORF4

<220>
<223> nirG gene

<400> 45
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tcgccttata gatagtgcgc cgagcagctt ggtgtggccg aggcggaatt gctggagagg 120
ctgcaaacct tgttgaacca gggcggttta tcgcgctttg ggccgatgta tcacgccgag 180
caaatgggag gcgccttgac cttggcggcg atgaagggtgc caggggagcg ttccgacgaa 240
attgcaggca tcgtcaacgg ctttccggag gtggcgcata actatgcgcg taaccacgcc 300
ttgaacatgt ggtttgtgtt ggcgaccgaa aagccggaac aagtgcaggc ggtcatcgat 360
gccatcgaac ggcaaactgg cttgacggtc tataacatgc cgaaaatcaa ggaatattac 420
gtgggcttgc aactggaggc c 441

<210> 46
<211> 147
<212> PRT
<213> *Methylobacterium* 16a

<220>
<223> NirG

<400> 46
Met Asp Asp Ile Asp Lys Ala Ile Ile Asn Arg Leu Gln Gln Gly Leu
1 5 10 15
Pro Ile Cys Glu Ser Pro Tyr Arg Tyr Val Ala Glu Gln Leu Gly Val
20 25 30
Ala Glu Ala Glu Leu Leu Glu Arg Leu Gln Thr Leu Leu Asn Gln Gly
35 40 45
Val Leu Ser Arg Phe Gly Pro Met Tyr His Ala Glu Gln Met Gly Gly
50 55 60
Ala Leu Thr Leu Ala Ala Met Lys Val Pro Gly Glu Arg Phe Asp Glu
65 70 75 80
Ile Ala Gly Ile Val Asn Gly Phe Pro Glu Val Ala His Asn Tyr Ala
85 90 95
Arg Asn His Ala Leu Asn Met Trp Phe Val Leu Ala Thr Glu Lys Pro
100 105 110
Glu Gln Val Gln Ala Val Ile Asp Ala Ile Glu Arg Gln Thr Gly Leu
115 120 125
Thr Val Tyr Asn Met Pro Lys Ile Lys Glu Tyr Tyr Val Gly Leu Gln
130 135 140

Leu Glu Ala
145

<210> 47
<211> 498
<212> DNA
<213> *Methylobacter* 16a

<220>
<223> ORF5

<220>
<223> nirH gene

<400> 47
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accaggccg gcttgccgct ggtcgcgga ccttatcagg ccgtcgccga gcaattgggc 120
atcacggctc aagaattgat gctgcgcatg gccgatatgc tggaagctgg catcattcgg 180
cggattgcgg cggtgccgaa tcattacaaa ctgggttatc gtcataacgg catgacgggc 240
tgggatgtcg atgaccggca tgtcgacagc ctggggcagc gcgtcgccga attgccgttc 300
gtcagtcatt gctaccaacg gcctcgccat ttgccggatt ggccgtataa cctgttcgcg 360
atggtgcatg gcaagacgga acaagacgcc gaaaaacaaa ttgccgtgat cgccgaattg 420
ttgggcgagg attgctaccg gcacgcggtg ctgtacagca ccaagatttt gaagaaaacc 480
ggcttgagga ttgcggggg 498

<210> 48
<211> 166
<212> PRT
<213> *Methylobacter* 16a

<220>
<223> NirH

<400> 48
Met Asp Ser Glu Pro Val Lys Ile Met Ile Asp Thr Ile Asp Arg Gln
1 5 10 15
Ile Ile Gln Ala Thr Gln Ala Gly Leu Pro Leu Val Ala Glu Pro Tyr
20 25 30
Gln Ala Val Ala Glu Gln Leu Gly Ile Thr Ala Gln Glu Leu Met Leu
35 40 45
Arg Met ala Asp Met Leu Glu Ala Gly Ile Ile Arg Arg Ile Ala Ala
50 55 60
Val Pro Asn His Tyr Lys Leu Gly Tyr Arg His Asn Gly Met Thr Val
65 70 75 80
Trp Asp Val Asp Asp Arg His Val Asp Ser Leu Gly Gln Arg Val Ala
85 90 95
Glu Leu Pro Phe Val Ser His Cys Tyr Gln Arg Pro Arg His Leu Pro
100 105 110
Asp Trp Pro Tyr Asn Leu Phe Ala Met Val His Gly Lys Thr Glu Gln
115 120 125
Asp Ala Glu Lys Gln Ile Ala Val Ile Ala Glu Leu Leu Gly Glu Asp
130 135 140

Cys Tyr Arg His Ala Val Leu Tyr Ser Thr Lys Ile Leu Lys Lys Thr
 145 150 155 160

Gly Leu Arg Ile Ala Gly
 165

<210> 49
 <211> 1137
 <212> DNA
 <213> *Methylobacter* 16a

<220>
 <223> ORF6

<220>
 <223> nirJ gene

<400> 49
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 cgaaaccgt ccggcccgtt ggtaatcttg aatctgatcc gtcgctgcaa cctgacttgc 120
 aagcattgct ataccacgtc cgccgacatc gattttccgg gtgaactgac gacgccggaa 180
 atttatgcgg tgatggacga tttgaaagcc ttcaaggtgc cgggtattgat tctgtccggc 240
 ggagagccgt tgctgcatcc ggatattttt ccgatttgcg aacgcgccag cgacatgggc 300
 ttttacgtgg ccttgtccag caacggcacg ctgatcgaca aaaacaatat cgagcaaadc 360
 gccgcgatcg attatcaata tattggcgct agtctggacg gcatgcgcga ggcgcacgac 420
 aagttccgcc agaagcaagg ctctttcgac gcctcgctgg ccggcatccg tttatgccgc 480
 gagcatggca tcaaggccgg cgtgcgcttc acgttgacgc gggacaacgc tcacgatttc 540
 gatgccttgc tgcagttgat ggacgaggag gacatcgaca aattctatct gtcgcatctg 600
 aattacggcg gccgcggcaa taaaaaccgg aaagacgatg ccgagtttca gttgaccgcg 660
 aaggtcatgg acgccttgtt cgaaaaggcg ctgagctggg aacagcaagg cctacaccgc 720
 gaagtgggtc ccggcaacaa cgatgccgat gccgtatatt tctgcatctg ggtcaaaccg 780
 cgctttcccg agcgcgccga gcatatccag gccaaagttg agcaatgggg cggcaatgct 840
 tccggcgctc acgtagccaa tatcgataat ctgggtaacg tgcacccga taccttttgg 900
 tggcattaca acttgggcag tgtccgccag cggccggttt ccgagatatg gcaggatgtg 960
 tccgacccat tgatggccgg gctgaaggcc tcgccgcgcc cgctgaaagg ccgctgcggc 1020
 acctgtcatt atcaaagcat ttgcaacggc aataccgcgc tccgcgcca acaactgacc 1080
 ggcgattttt gggctgaaga tccaggctgc tacctggatg acgaggaagt tttcagc 1137

<210> 50
 <211> 379
 <212> PRT
 <213> *Methylobacter* 16a

<220>
 <223> Nir J

<400> 50
 Met Phe Arg Leu Ser Gln Tyr Met Arg Glu Leu Val His Ser Thr Pro
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 Leu Gly Lys Pro Arg Lys Pro Ser Gly Pro Val Val Ile Trp Asn Leu
 20 25 30
 Ile Arg Arg Cys Asn Leu Thr Cys Lys His Cys Tyr Thr Thr Ser Ala
 35 40 45
 Asp Ile Asp Phe Pro Gly Glu Leu Thr Thr Pro Glu Ile Tyr Ala Val
 50 55 60

Met	Asp	Asp	Leu	Lys	Ala	Phe	Lys	Val	Pro	Val	Leu	Ile	Leu	Ser	Gly	65	70	75	80
Gly	Glu	Pro	Leu	Leu	His	Pro	Asp	Ile	Phe	Pro	Ile	Ser	Gln	Arg	Ala		85	90	95
Ser	Asp	Met	Gly	Phe	Tyr	Val	Ala	Leu	Ser	Ser	Asn	Gly	Thr	Leu	Ile	100	105		110
Asp	Lys	Asn	Asn	Ile	Glu	Gln	Ile	Ala	Ala	Ile	Asp	Tyr	Gln	Tyr	Ile	115	120		125
Gly	Val	Ser	Leu	Asp	Gly	Met	Arg	Glu	Ala	His	Asp	Lys	Phe	Arg	Gln	130	135		140
Lys	Gln	Gly	Ser	Phe	Asp	Ala	Ser	Leu	Ala	Gly	Ile	Arg	Leu	Cys	Arg	145	150	155	160
Glu	His	Gly	Ile	Lys	Ala	Gly	Val	Arg	Phe	Thr	Leu	Thr	Arg	Asp	Asn		165	170	175
Ala	His	Asp	Phe	Asp	Ala	Leu	Leu	Gln	Leu	Met	Asp	Glu	Glu	Asp	Ile	180		185	190
Asp	Lys	Phe	Tyr	Leu	Ser	His	Leu	Asn	Tyr	Gly	Gly	Arg	Gly	Asn	Lys	195	200		205
Asn	Arg	Lys	Asp	Asp	Ala	Glu	Phe	Gln	Leu	Thr	Arg	Lys	Val	Met	Asp	210	215		220
Ala	Leu	Phe	Glu	Lys	Ala	Leu	Ser	Trp	Glu	Gln	Gln	Gly	Leu	His	Arg	225	230	235	240
Glu	Val	Val	Thr	Gly	Asn	Asn	Asp	Ala	Asp	Ala	Val	Tyr	Phe	Leu	His		245	250	255
Trp	Val	Lys	Arg	Arg	Phe	Pro	Glu	Arg	Ala	Glu	His	Ile	Gln	Ala	Lys	260	265		270
Leu	Gln	Gln	Trp	Gly	Gly	Asn	Ala	Ser	Gly	Val	Asn	Val	Ala	Asn	Ile	275	280		285
Asp	Asn	Leu	Gly	Asn	Val	His	Pro	Asp	Thr	Phe	Trp	Trp	His	Tyr	Asn	290	295	300	
Leu	Gly	Ser	Val	Arg	Gln	Arg	Pro	Phe	Ser	Glu	Ile	Trp	Gln	Asp	Val	305	310	315	320
Ser	Asp	Pro	Leu	Met	ala	Gly	Leu	Lys	Ala	Ser	Pro	Arg	Pro	Leu	Lys		325	330	335
Gly	Arg	Cys	Gly	Thr	Cys	His	Tyr	Gln	Ser	Ile	Cys	Asn	Gly	Asn	Thr	340	345		350
Arg	Val	Arg	Ala	Gln	Gln	Leu	Thr	Gly	Asp	Phe	Trp	Ala	Glu	Asp	Pro	355	360		365
Gly	Cys	Tyr	Leu	Asp	Asp	Glu	Glu	Val	Phe	Ser						370	375		

<210> 51
 <211> 2760
 <212> DNA
 <213> *Methylobionas* 16a

<220>
 <223> ORF7

<220>
 <223> nasA gene

<400> 51
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 gccagggtgc tcgatgccga aaaccatgtc gtcaatattg ccggcgatcc acagcatcag 120
 tccaatttcg gccgactgtg ctccaagggc gggcgctggg gtgataccgt cggctcggaa 180
 ggccgccttt tatacccga aatcgatggc cggcgctggg attggccac ggtgctggac 240
 cggatcgccg cttaaattcaa tgcgatcatt gccgagcac gcccggacgc ggtggcgttt 300
 tatgtgtccg gacagttgtt gaccgaggat tattatgtcg ccaacaaatt gatgaagggc 360
 ttcacgggtt cggcgaatat cgataccaat tccaggctgt gcatgtcctc ggcggtagtc 420
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 atcttcaagg aacacgcggc cttgtccggt tttgaaaatg atgcagcgca ggggggagc 1560
 gatttttgata tttcaggcct ggcaacgctg gatcaggccc agtttgacgc cttagtgcgc 1620
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 cacacgatga cccgcaccgc gctgtccgag aagctcaatc aacacaagcc ggaaccgttc 1860
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 atcgaaagcc gttggggcgg catgttggcg cgggtcgacg tcagcgaggc tcagcaacc 1980
 ggcagcgtgt tcgtgcccac gcaactggac gccagctca gcagtcattg ccgagtcggc 2040
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 ttgccggacc ctggctgggt ggccagccta ttcggcaaac cgagattgac ccgcaaggaa 2460
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 agctgtgtaa cagatatagg caactgcctg catgcgggaa cgggttgtgg ttcgtgttta 2640
 ccggaattaa aaagcatttt ggcccacgcc aaaacgatcg atcctgcctc gctgccatt 2700
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<210> 52
 <211> 920
 <212> PRT
 <213> *Methylobacter* 16a

<220>
 <223> NasA

<400> 52

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Cys	Gly	Ile	Glu	Ala	Arg	Val	Leu	Asp	Ala	Glu	Asn	His	Val	Val	Asn
			20					25					30		
Ile	Ala	Gly	Asp	Pro	Gln	His	Gln	Ser	Asn	Phe	Gly	Arg	Leu	Cys	Ser
		35					40					45			
Lys	Gly	Ala	Ala	Leu	Gly	Asp	Thr	Val	Gly	Leu	Glu	Gly	Arg	Leu	Leu
	50					55					60				
Tyr	Pro	Glu	Ile	Asp	Gly	Arg	Arg	Val	Asp	Trp	Pro	Thr	Val	Leu	Asp
65					70				75						80
Arg	Ile	Ala	Ala	Lys	Phe	Asn	Ala	Ile	Ile	Ala	Glu	His	Gly	Pro	Asp
				85					90					95	
Ala	Val	Ala	Phe	Tyr	Val	Ser	Gly	Gln	Leu	Leu	Thr	Glu	Asp	Tyr	Tyr
			100					105					110		
Val	Ala	Asn	Lys	Leu	Met	Lys	Gly	Phe	Ile	Gly	Ser	Ala	Asn	Ile	Asp
		115					120					125			
Thr	Asn	Ser	Arg	Leu	Cys	Met	Ser	Ser	Ala	Val	Val	Gly	Tyr	Lys	Arg
	130					135					140				
Ala	Phe	Gly	Ala	Asp	Ala	Val	Pro	Cys	Asn	Phe	Glu	Asp	Leu	Glu	Arg
145					150					155					160
Ala	Asp	Leu	Ile	Val	Leu	Val	Gly	Ser	Asn	Ala	Ala	Trp	Cys	His	Pro
				165					170					175	
Ile	Ala	Phe	Gln	Arg	Met	Arg	Gln	Ala	Lys	Ile	Asp	Asn	Pro	Ala	Leu
			180					185					190		
Lys	Ile	Val	Leu	Ile	Asp	Pro	Arg	Gln	Thr	Ser	Ser	Cys	Asp	Ile	Ala
		195					200					205			
Asp	Arg	His	Leu	Ala	Ile	Lys	Pro	Gly	Met	Asp	Gly	Leu	Leu	Phe	Asn
	210					215					220				
Gly	Leu	Leu	Val	Tyr	Leu	Ala	Glu	Thr	Gly	Ala	Leu	Asp	Gln	Asp	Tyr
225					230					235					240
Ile	Glu	Arg	His	Cys	Glu	Gly	Phe	Ala	Glu	Ala	Leu	Ala	Thr	Ala	Arg
				245					250					255	
Ala	Ser	Ala	Ala	Asp	Phe	Thr	Val	Leu	Ala	Asn	Arg	Cys	Gly	Val	Ala
			260					265					270		

Ala	His	Asp	Leu	Ala	Gln	Leu	Phe	Ala	Trp	Phe	Ala	Gly	Leu	Asp	Lys	275	280	285
Val	Val	Thr	Val	Tyr	Ser	Gln	Gly	Ile	Asn	Gln	Ser	Ser	Ser	Gly	Ser	290	295	300
Asp	Lys	Cys	Asn	Ala	Ile	Ile	Asn	Cys	His	Leu	Ala	Ser	Gly	Lys	Ile	305	310	315
Gly	Lys	Pro	Gly	Cys	Gly	Pro	Phe	Ser	Phe	Thr	Gly	Gln	Pro	Asn	Ala	325	330	335
Met	Gly	Gly	Arg	Glu	Val	Gly	Gly	Leu	Ala	Asn	Met	Leu	Ala	Ala	His	340	345	350
Met	Asp	Leu	Glu	Asn	Pro	Ala	His	Val	Asp	Arg	Val	Ala	Arg	Phe	Trp	355	360	365
Gln	Thr	Asp	Ser	Val	Ala	Arg	Lys	Pro	Gly	Leu	Lys	Ala	Val	Glu	Ile	370	375	380
Phe	Asp	Ala	Ile	Ala	Asp	Gly	Arg	Ile	Lys	Ala	Leu	Trp	Ile	Met	ala	385	390	395
Thr	Asn	Pro	Val	Val	Ser	Met	Pro	Asp	Ala	Asp	Lys	Val	Ile	Glu	Ala	405	410	415
Leu	Lys	Gln	Cys	Glu	Phe	Leu	Leu	Val	Ser	Asp	Cys	Ile	Ala	Asn	Thr	420	425	430
Asp	Thr	Val	Glu	Leu	Ala	His	Val	Lys	Leu	Pro	Ala	Thr	Gly	Trp	Ser	435	440	445
Glu	Lys	Asp	Gly	Thr	Val	Thr	Asn	Leu	Glu	Arg	Arg	Ile	Ser	Arg	Gln	450	455	460
Arg	Pro	Leu	Phe	Gln	Pro	Ser	Gly	Glu	Ala	Lys	Pro	Asp	Trp	Trp	Ile	465	470	475
Val	Ser	Gln	Val	Ala	Lys	Arg	Met	Gly	Phe	Ala	Gly	Phe	Asp	Tyr	Arg	485	490	495
Asn	Ser	Ala	Glu	Ile	Phe	Lys	Glu	His	Ala	Ala	Leu	Ser	Gly	Phe	Glu	500	505	510
Asn	Asp	Ala	Ala	Gln	Gly	Gly	Arg	Asp	Phe	Asp	Ile	Ser	Gly	Leu	Ala	515	520	525
Thr	Leu	Asp	Gln	Ala	Gln	Phe	Asp	Ala	Leu	Val	Pro	Ile	Gln	Trp	Pro	530	535	540
Val	Thr	Gly	Lys	Thr	Gln	Gly	Gly	Thr	Ala	Arg	Leu	Phe	Glu	Asp	Gly	545	550	555
Arg	Phe	Phe	Thr	Asp	Thr	Gly	Lys	Ala	Arg	Phe	Ile	Ala	Leu	Glu	Pro	565	570	575
Arg	Ser	Pro	Met	His	Ala	Pro	Thr	Pro	Asp	Tyr	Pro	Leu	Val	Leu	Asn	580	585	590

Thr	Gly	Arg	Ile	Arg	Asp	Gln	Trp	His	Thr	Met	Thr	Arg	Thr	Ala	Leu	595	600	605	
Ser	Ala	Lys	Leu	Asn	Gln	His	Lys	Pro	Glu	Pro	Phe	Val	Glu	Ile	His	610	615	620	
Pro	Gln	Asp	Ala	Leu	Arg	Trp	Gly	Leu	Lys	Ala	Asn	Ala	Leu	Ala	Arg	625	630	635	640
Ile	Glu	Ser	Arg	Trp	Gly	Gly	Met	Leu	Ala	Arg	Val	Asp	Val	Ser	Glu	645	650	655	
Ala	Gln	Gln	Pro	Gly	Ser	Val	Phe	Val	Pro	Met	His	Trp	Thr	Ala	Gln	660	665	670	
Leu	Ser	Ser	His	Gly	Arg	Val	Gly	Ala	Val	Val	Asn	Pro	Val	Val	Asp	675	680	685	
Pro	Leu	Ser	Gly	Gln	Pro	Glu	Ser	Lys	Gln	Thr	Pro	Val	Arg	Ile	Ala	690	695	700	
Ala	Trp	Ala	Pro	Cys	Trp	Gln	Ala	Met	Val	Leu	Thr	Lys	Met	Pro	Leu	705	710	715	720
Asp	Ile	Asp	Asp	Cys	Glu	Tyr	His	Val	Lys	Ile	Arg	Gly	His	Gly	Phe	725	730	735	
Trp	Arg	Tyr	His	Leu	Ala	Asp	Gln	Ser	Gln	Arg	Pro	Asp	Leu	Pro	Ala	740	745	750	
Trp	Gly	Arg	Gly	Ile	Val	Gly	Arg	Gly	Ala	Ala	Lys	Pro	Asn	Asp	Cys	755	760	765	
Val	Glu	Tyr	Leu	Asp	Leu	Ala	Ala	Gly	Asp	Tyr	Arg	Phe	Ala	Glu	Met	770	775	780	
Arg	Asp	Gln	Thr	Leu	His	Ala	Cys	Met	Phe	Ile	Thr	His	Asn	Gly	Glu	785	790	795	800
Leu	Pro	Asp	Pro	Gly	Trp	Leu	Ala	Ser	Leu	Phe	Gly	Lys	Pro	Arg	Leu	805	810	815	
Thr	Arg	Lys	Glu	Arg	Phe	Asn	Leu	Leu	Ser	Gly	Val	Pro	Pro	Gln	Gly	820	825	830	
Glu	Ile	Asp	Ser	Gly	Lys	Thr	Ile	Cys	Ser	Cys	Phe	Asn	Val	Gly	Glu	835	840	845	
Lys	Thr	Ile	Val	Gln	Ala	Ile	Gln	Thr	Arg	His	Leu	Ser	Cys	Val	Thr	850	855	860	
Asp	Ile	Gly	Asn	Cys	Leu	His	Ala	Gly	Thr	Gly	Cys	Gly	Ser	Cys	Leu	865	870	875	880
Pro	Glu	Leu	Lys	Ser	Ile	Leu	Ala	His	Ala	Lys	Thr	Ile	Asp	Pro	Ala	885	890	895	
Ser	Leu	Pro	Ile	Gln	Pro	Thr	Gln	Ile	Pro	Pro	Ala	Ser	Glu	Gly	Lys	900	905	910	

Glu Glu Ala Phe Phe Ser Gly Gln
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 <212> DNA
 <213> *Methylobacter* 16a

<220>
 <223> ORF8

<220>
 <223> norC gene

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 gtgttgctgg tgatcttgac cttcgactcg ctggcgaaga tttccgctgg cggccccagg 180
 gtgcccgcct tcgacgtcat caacaaagac gtcagttacc gtttcgacaa ggaaaaacaa 240
 cgctaccaac cagtgatcgg cgacgacgcc cctctgtttg gcaaaaccct gagcgaggaa 300
 gaagccgaaa aactggtcga cctgggcaag aaaaccgtgc aggccaaaga ctgcatgaac 360
 tgccataccc tgctcggcaa tggcgcttat tatgcgcccg acttgaccaa ggcctggctg 420
 gaccagggct ggatcgccaa ggagtcgcgc gagcaaatga tgggtcaattt cctgctcgat 480
 cccgagaaaa atgcccgcac cttegggtcc aaccgcaaga tgccgaatct cgacatcacg 540
 caacaggagg ccgagggcat cgtcgccctt ttgaaatgga tggcatccat cgacaccaat 600
 ggttttcgcg ataatttcac cgcgctgggc gaagaggaca aa 642

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 <212> PRT
 <213> *Methylobacter* 16a

<220>
 <223> NorC

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 Ile Trp Val Thr Gly Gly Ser Phe Val Leu Leu Val Ile Leu Thr Phe
 35 40 45
 Asp Ser Leu Ala Lys Ile Ser Ala Gly Gly Pro Arg Val Pro Ala Phe
 50 55 60
 Asp Val Ile Asn Lys Asp Val Ser Tyr Arg Phe Asp Lys Glu Lys Gln
 65 70 75 80
 Arg Tyr Gln Pro Val Ile Gly Asp Asp Ala Pro Leu Phe Gly Lys Thr
 85 90 95
 Leu Ser Glu Glu Glu Ala Glu Lys Leu Val Asp Leu Gly Lys Lys Thr
 100 105 110
 Val Gln Ala Lys Asn Cys Met Asn Cys His Thr Leu Leu Gly Asn Gly
 115 120 125

Ala Tyr Tyr Ala Pro Asp Leu Thr Lys Ala Trp Leu Asp Gln Gly Trp
130 135 140

Ile Ala Lys Glu Ser Arg Glu Gln Met Met Val Asn Phe Leu Leu Asp
145 150 155 160

Pro Glu Lys Asn Ala Arg Thr Phe Gly Ser Asn Arg Lys Met Pro Asn
165 170 175

Leu Asp Ile Thr Gln Gln Glu Ala Glu Gly Ile Val Ala Phe Leu Lys
180 185 190

Trp Met ala Ser Ile Asp Thr Asn Gly Phe Pro His Asn Phe Ile Ala
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Leu Gly Glu Glu Asp Lys
210

<210> 55
<211> 1503
<212> DNA
<213> *Methylobacterium* 16a

<220>
<223> ORF9

<220>
<223> norB gene

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ttcacgcgtc ccatgggtgt gttcatggcg caattgctgt tcggcctgct ggccggcctg 180
caattcatct tcccagagttt ttatatacgaa atcctggatt tcaacgtcaa ccgcatgggtg 240
cacatcaatg ccatgggtgt gtggatgctg tacggctttt tgggctcggg gtactgggtt 300
ctggaagacg agagcggcgt cgagatcgct ggcttgaaat gggggcaact ggcgttttg 360
gtgctgaccg gtgcgggtcg gctggctcgt ctgggtgatt tggatcatcca gatcggcgc 420
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attccgctgg tagcaatggc cgtgcattcc atttacgatt ccggcgtgca caagtttaaa 960
aacagcaatc accccgccct ggcctggatc atcgcccata ctttcggcaa cttcctgggc 1020
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gaa 1503

<210> 56
<211> 501

<212> PRT
 <213> *Methylobionas* 16a

<220>
 <223> NorB

<400> 56

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Gly	Gln	Lys	Leu	Ala	Val	His	Tyr	Phe	Thr	Val	Ala	Met	Val	Leu	Phe
		35					40					45			
Met	ala	Gln	Leu	Leu	Phe	Gly	Leu	Leu	Ala	Gly	Leu	Gln	Phe	Ile	Phe
	50					55					60				
Pro	Ser	Phe	Leu	Tyr	Glu	Ile	Leu	Asp	Phe	Asn	Val	Asn	Arg	Met	Val
	65				70					75					80
His	Ile	Asn	Ala	Met	Val	Val	Trp	Met	Leu	Tyr	Gly	Phe	Leu	Gly	Ser
				85					90					95	
Val	Tyr	Trp	Phe	Leu	Glu	Asp	Glu	Ser	Gly	Val	Glu	Ile	Val	Gly	Leu
			100					105					110		
Lys	Trp	Gly	Gln	Leu	Ala	Phe	Trp	Val	Leu	Thr	Gly	Ala	Val	Ala	Leu
		115					120					125			
Val	Val	Leu	Val	Tyr	Leu	Phe	Ile	Gln	Ile	Gly	Ala	Gly	Asn	Asp	Thr
	130					135					140				
Ser	Leu	Trp	Leu	Ile	Asn	Glu	Gly	Arg	Glu	Tyr	Ile	Glu	Ala	Pro	Arg
145					150					155					160
Trp	Ala	Asp	Ile	Gly	Ile	Val	Ala	Val	Val	Leu	Thr	Phe	Phe	Tyr	Asn
			165						170					175	
Val	Ala	Ala	Thr	Phe	Ala	Lys	Gly	Lys	Trp	Ser	Gly	Ile	Ala	Gly	Val
			180					185					190		
Leu	Thr	Leu	Asp	Leu	Val	Ala	Leu	Ala	Gly	Leu	Tyr	Leu	Ala	Gly	Met
		195					200					205			
Phe	Tyr	Val	Thr	Asn	Ile	Ser	Val	Asp	Gln	Tyr	Trp	Trp	Trp	Trp	Val
	210				215						220				
Ile	His	Leu	Trp	Val	Glu	Ala	Thr	Trp	Glu	Val	Leu	Val	Gly	Cys	Ile
225					230					235				240	
Met	ala	Trp	Ser	Leu	Met	Lys	Leu	Leu	Gly	Val	Arg	Arg	Gln	Val	Val
			245						250					255	
Gln	Thr	Trp	Leu	Tyr	Ile	Glu	Val	Ala	Leu	Met	Phe	Gly	Ser	Gly	Ile
			260					265					270		
Leu	Gly	Leu	Gly	His	His	Tyr	Phe	Trp	Ile	Gly	Thr	Pro	Glu	Tyr	Trp
	275						280					285			

Phe Ser Ile Gly Gly Phe Phe Ser Ala Leu Glu Pro Ile Pro Leu Val
 290 295 300
 Ala Met Val Val His Ser Ile Tyr Asp Ser Gly Val His Lys Phe Lys
 305 310 315 320
 Asn Ser Asn His Pro Ala Leu Ala Trp Ile Ile Ala His Thr Phe Gly
 325 330 335
 Asn Phe Leu Gly Ala Gly Val Trp Gly Phe Met His Thr Leu Pro Gln
 340 345 350
 Ile Asn Leu Tyr Thr His Gly Thr Gln Trp Ser Ala Ser His Gly His
 355 360 365
 Leu Ala Phe Phe Gly Ala Tyr Ala Thr Ile Asn Ile Ala Phe Phe Tyr
 370 375 380
 Leu Ala Ala Gln Gln Ala Arg Gly Asn Val Trp Met Gly Gly Asp Leu
 385 390 395 400
 Ile Asn Gly Trp Arg Trp Lys Ala Ala Ala Ile Leu Leu Asn Leu Gly
 405 410 415
 Val Leu Gly Met Thr Val Ala Leu Leu Ile Ala Gly Tyr Glu Gln Ser
 420 425 430
 Phe Ile Glu Arg Ala Val Glu Gly Ser Thr Trp Ala Gly Tyr Phe Ala
 435 440 445
 Ala Gln Asn His Pro Trp Phe Met Gln Ala Met Val Trp Arg Met Val
 450 455 460
 Phe Gly Leu Met Thr Ala Val Gly Gly Gly Leu Leu Phe Trp Asp Leu
 465 470 475 480
 Leu Glu Ile Gly Lys Gly Glu Gln Arg Pro Ala Ala Val Ile Ala Gly
 485 490 495
 Gly Thr Val Ala Glu
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<210> 57
 <211> 2253
 <212> DNA
 <213> *Methylobionas* 16a

<220>
 <223> ORF10

<220>
 <223> norZ gene

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 ccggcccaaa tcgttgatgc acaagggtgtt cgcctgtttt ccgggtgacga aatcaaagaa 180
 ggccaggcta tctttctcaa atacgggttg atgaacaacg gcagtatctg gggatcatggc 240
 gcataacttg ggccagatta ttcggccgag gcattgcacc gaatcggcga gaacaccgcc 300

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actatcattg cccagcagca ataccaacag ccactttcct cactcacgcc cggccaattg 360
gccgccgtgt atgcacaaac cgcagtcgag cttaaagacca atcattatga tgccgccagc 420
gcaacgttgc gtctgaccgt gccggagaca tccgcctatc gtaagcagat cgcttattgg 480
acggattatt tcctgaatcc tgaacggaat ggcggactca aacgtggatt gatcagcgat 540
ccgactgaac tgcgccagtt taccgccttc atcacatgga ctgcctgggc ctcggtggcc 600
aaccgccccg gcgagaacta ctctacacc aacaattttc catacgaccc cagcgtcggg 660
aatatgcccc ttcccgggtgc gctgttatgg agtgcgttga gccttatcgt gctgctggcc 720
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<210> 48
<211> 751
<212> PRT
<213> Methylobionas 16a

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<220>
<223> NorZ

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Ala Tyr Arg Asn Ala Pro Pro Ile Pro Ala Gln Ile Val Asp Ala Gln
      35                40                45

Gly Val Arg Leu Phe Ser Gly Asp Glu Ile Lys Glu Gly Gln Ala Ile
      50                55                60

Phe Leu Lys Tyr Gly Leu Met Asn Asn Gly Ser Ile Trp Gly His Gly
      65                70                75                80

Ala Tyr Leu Gly Pro Asp Tyr Ser Ala Glu Ala Leu His Arg Ile Gly
      85                90                95

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Glu	Asn	Thr	Ala	Thr	Ile	Ile	Ala	Gln	Gln	Gln	Tyr	Gln	Gln	Pro	Leu		
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Ser	Ser	Leu	Thr	Pro	Gly	Gln	Leu	Ala	Ala	Val	Tyr	Ala	Gln	Thr	Ala		
		115					120					125					
Val	Glu	Leu	Lys	Thr	Asn	His	Tyr	Asp	Ala	Ala	Ser	Ala	Thr	Leu	Arg		
	130					135					140						
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145					150					155					160		
Thr	Asp	Tyr	Phe	Leu	Asn	Pro	Glu	Arg	Asn	Gly	Gly	Leu	Lys	Arg	Gly		
				165					170					175			
Leu	Ile	Ser	Asp	Pro	Thr	Glu	Leu	Arg	Gln	Phe	Thr	Ala	Phe	Ile	Thr		
			180					185					190				
Trp	Thr	Ala	Trp	Ala	Ser	Val	Ala	Asn	Arg	Pro	Gly	Glu	Asn	Tyr	Ser		
		195					200					205					
Tyr	Thr	Asn	Asn	Phe	Pro	Tyr	Asp	Pro	Ser	Val	Gly	Asn	Met	Pro	Val		
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Pro	Gly	Ala	Leu	Leu	Trp	Ser	Ala	Leu	Ser	Leu	Ile	Val	Leu	Leu	Ala		
225					230					235					240		
Gly	Ile	Gly	Ile	Val	Leu	Leu	Met	Phe	Gly	Lys	Phe	Asp	Tyr	Leu	Gly		
				245					250					255			
Trp	Ile	Ser	Thr	Gly	His	His	Val	His	Pro	His	Leu	Leu	Pro	Gly	Gln		
			260					265					270				
Ala	Ser	Ala	Gly	Gln	Leu	Ala	Leu	Val	Lys	Phe	Phe	Val	Val	Val	Ala		
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Leu	Leu	Phe	Leu	Ala	Gln	Thr	Leu	Val	Gly	Gly	Ala	Thr	Ala	His	Tyr		
	290					295					300						
Arg	Ala	Asp	Pro	Gly	Ser	Phe	Tyr	Gly	Leu	Glu	Leu	Glu	Lys	Leu	Phe		
305					310					315					320		
Pro	Ser	Asn	Leu	Met	Arg	Thr	Trp	His	Leu	Gln	Thr	Ala	Val	Phe	Trp		
			325						330					335			
Ile	Ala	Thr	Ala	Phe	Val	Ala	Ala	Ala	Leu	Phe	Leu	Gly	Arg	Ser	Leu		
			340					345					350				
Arg	Asn	Asp	Glu	Pro	Arg	Trp	Phe	Ala	Gly	Trp	Val	His	Leu	Leu	Phe		
		355					360					365					
Gly	Ala	Phe	Ala	Val	Val	Ile	Gly	Gly	Ser	Leu	Leu	Gly	Glu	Trp	Ala		
	370					375					380						
Gly	Ile	Ser	Gln	Met	Leu	Asp	Gln	Trp	Trp	Phe	Trp	Leu	Gly	Asn	Gln		
385					390					395					400		
Gly	Trp	Glu	Tyr	Leu	Glu	Leu	Gly	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ile		
				405					410					415			

Ala	Gly	Leu	Leu	Ala	Trp	Phe	Thr	Leu	Leu	Phe	Lys	Leu	Leu	Gln	Pro	
			420					425						430		
Asp	Thr	Leu	Asn	Asp	Ser	Glu	Ala	Lys	Pro	Leu	Val	Arg	Leu	Phe	Leu	
		435					440					445				
Leu	Ala	Ser	Leu	Ala	Ile	Pro	Leu	Phe	Tyr	Ile	Pro	Ala	Leu	Phe	Phe	
	450					455					460					
Gly	Ala	Lys	Thr	Asn	Phe	Thr	Val	Val	Asp	Thr	Trp	Arg	Phe	Trp	Ile	
465					470					475					480	
Ile	His	Leu	Trp	Val	Glu	Gly	Phe	Phe	Glu	Phe	Phe	Ala	Thr	Thr	Leu	
				485					490					495		
Val	Ala	Leu	Leu	Phe	Tyr	Gln	Leu	Gly	Leu	Thr	Gln	Arg	Asn	Val	Ala	
			500					505					510			
Leu	Arg	Val	Ile	Tyr	Leu	Asp	Ala	Ile	Leu	Tyr	Phe	Val	Gly	Gly	Leu	
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Ile	Gly	Thr	Gly	His	His	Trp	Tyr	Phe	Thr	Gly	Gln	Ser	Ser	Val	Asn	
	530					535					540					
Met	ala	Leu	Ser	Ala	Met	Val	Ser	Val	Leu	Glu	Val	Val	Pro	Leu	Thr	
545					550					555					560	
Leu	Leu	Thr	Leu	Asp	Ala	Trp	Asp	Phe	Val	Arg	Thr	Thr	Arg	Ala	Asp	
				565					570					575		
Cys	Asp	Val	Cys	Gly	Lys	Pro	Val	Ala	Ile	Pro	His	Lys	Trp	Thr	Phe	
			580					585					590			
Tyr	Phe	Leu	Met	ala	Val	Gly	Phe	Trp	Asn	Phe	Val	Gly	Ala	Gly	Ile	
		595					600					605				
Phe	Gly	Phe	Leu	Ile	Asn	Leu	Pro	Ile	Val	Ser	Tyr	Tyr	Glu	Val	Gly	
	610					615					620					
Thr	Gln	Leu	Thr	Pro	Asn	His	Gly	His	Ala	Ala	Met	Met	Gly	Val	Phe	
625					630					635					640	
Gly	Met	Leu	Ala	Leu	Ala	Leu	Met	Val	Phe	Val	Leu	Arg	Gln	Thr	Ser	
				645					650					655		
Ser	Asp	Leu	Arg	Trp	Val	Asp	Ile	Glu	Lys	Tyr	Val	Arg	Val	Gly	Phe	
			660					665					670			
Trp	Gly	Ser	Asn	Val	Gly	Leu	Ala	Leu	Met	Leu	Ile	Met	Ser	Leu	Phe	
		675					680					685				
Pro	Ser	Gly	Val	Leu	Gln	Val	Trp	Asp	Val	Val	Gln	His	Gly	Tyr	Trp	
		690				695					700					
His	Ala	Arg	Ser	Leu	Asp	Tyr	Ile	Gly	Ser	Glu	Arg	Ser	Arg	Leu	Ile	
705					710					715					720	
Glu	Trp	Leu	Arg	Leu	Pro	Gly	Asp	Leu	Val	Phe	Ile	Leu	Phe	Gly	Ala	
				725					730					735		

Ile Pro Leu Ala Ile Ala Ser Ile Lys Gly Trp Leu Asp Val His
740 745 750

<210> 59
<211> 1581
<212> DNA
<213> *Methylobacterium* 16a

<220>
<223> ORF11

<220>
<223> norS gene

<400> 59
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gataattgcg ccagctgcca cggcgcgat cacggtggct atctggcgcc agccttgaat 180
gccgatacct tgaaagggtcg tagccctacg gcgttgcgta ccacgtcat ggccggcagc 240
ttcgatacgc tgatgcctcc cttctacggc aaactgagcg acgacgagat tcgcggtcg 300
atcaagcatt tgcaggaaac ccgaaacag ccgaatccgg cctggaccat cgacgacatg 360
aagaagtcct tgaagggtta cgtcaaggat gagagcaccg tgctggcaa gccgactttc 420
caaactcgata acatcgataa tctgatcggc gtggcgccac gcggcaaata cggccgtggc 480
gaaggctcca aagctatctt catcaacagc accaaccatc aaaaagtcgg cgaagtggct 540
accggcaccg ccgcgcatat catcgacttc aatcctgcca acccgcgctg ggcttacgta 600
aaaaccgaca ccgccgagat tttcaaggta gatttgatt cgatgcaggc ggtccgcagc 660
atcaagacag gttacaacgg ccccgcatg ggggtatccc gcgacggcaa atacatcatg 720
gccggctcct tcgtgccgca taacgccgta atcctggatg ccgaaaccct ggaaccgttg 780
aaaaccttcg aactggaagg catcgatccc gacggtaaac atgtttcttc cgactcgggc 840
atgatcatcg gtacccttta tgccgacgtg ttcgcgattg cgctggaaaa tgccggccag 900
gtctggatcg tcgattacaa caaagaaggc ttcccgggtc caaaatcga gaaagtgggc 960
cgtcacttgc acgacgcctt cctgacgcat ggcggaaga aactgatggt ggcgctttat 1020
gacgacagca tcgtcgccgc gatcgatctg gaaaaacgag aactgatcaa gcaattgcca 1080
gcgggttggt tgccgcacgt cgggtggcggc gcggcggtcg tggttgatgg tcgtaccttg 1140
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aaaatggaag tcgtcaaaca agtaccggtt tcaggtggca ctgaatcgcc tcgggctcat 1260
gccaacgcac cttatgtcgc ggttgacatc atcagcaaag acagacgtgc acgcaccatt 1320
cagttgatcg acaagaaaac cctggaagtt gccaaaactc tggatgtcgg cggccacgcc 1380
tacttcccgg aatatagcgc cgacggcaaa ttcctctatg tcagtgcgg ctacaatggc 1440
gacgaagtcg tggtttacga ttccaatacc ttgcaaaaag tggcgaccgt gccgatggaa 1500
agtccgtgct gtatctttct cagaggccgt gtcaaatata tgactcgcg tctgtcacct 1560
gacgaaatgg agcaaggcaa a 1581

<210> 60
<211> 527
<212> PRT
<213> *Methylobacterium* 16a

<220>
<223> NorS

<400> 60
Met Met Lys Thr Thr Thr Lys Arg Arg Leu Asn Gln Ser Leu Leu Ala
1 5 10 15
Ser Ala Ile Ala Ala Leu Leu Ser Ser Gly Ala Val Leu Ala Lys Ser
20 25 30

Asp	Ser	Pro	His	Asp	Ile	Tyr	Met	Asp	Asn	Cys	Ala	Ser	Cys	His	Gly	35	40	45
Ala	Asp	His	Gly	Gly	Tyr	Leu	Ala	Pro	Ala	Leu	Asn	Ala	Asp	Thr	Leu	50	55	60
Lys	Gly	Arg	Ser	Pro	Thr	Ala	Leu	Arg	Thr	Ile	Val	Met	ala	Gly	Ser	65	70	75
Phe	Asp	Thr	Leu	Met	Pro	Pro	Phe	Tyr	Gly	Lys	Leu	Ser	Asp	Asp	Glu	85	90	95
Ile	Arg	Gly	Val	Ile	Lys	His	Leu	Gln	Glu	Thr	Pro	Lys	Gln	Pro	Asn	100	105	110
Pro	Ala	Trp	Thr	Ile	Asp	Asp	Met	Lys	Lys	Ser	Leu	Lys	Val	Tyr	Val	115	120	125
Lys	Asp	Glu	Ser	Thr	Leu	Pro	Gly	Lys	Pro	Thr	Phe	Gln	Ile	Asp	Asn	130	135	140
Ile	Asp	Asn	Leu	Ile	Gly	Val	Ala	Ala	Arg	Gly	Lys	Tyr	Gly	Arg	Gly	145	150	155
Glu	Gly	Ser	Lys	Ala	Ile	Phe	Ile	Asn	Ser	Thr	Asn	His	Gln	Lys	Val	165	170	175
Gly	Glu	Val	Ala	Thr	Gly	Thr	Ala	Ala	His	Ile	Ile	Asp	Phe	Asn	Pro	180	185	190
Ala	Asn	Pro	Arg	Trp	Ala	Tyr	Val	Lys	Thr	Asp	Thr	Ala	Glu	Ile	Phe	195	200	205
Lys	Val	Asp	Leu	Tyr	Ser	Met	Gln	Ala	Val	Arg	Ser	Ile	Lys	Thr	Gly	210	215	220
Tyr	Asn	Gly	Pro	Gly	Met	Gly	Val	Ser	Arg	Asp	Gly	Lys	Tyr	Ile	Met	225	230	235
Ala	Gly	Ser	Phe	Val	Pro	His	Asn	Ala	Val	Ile	Leu	Asp	Ala	Glu	Thr	245	250	255
Leu	Glu	Pro	Leu	Lys	Thr	Phe	Glu	Leu	Glu	Gly	Ile	Asp	Pro	Asp	Gly	260	265	270
Lys	His	Val	Ser	Ser	Asp	Ser	Gly	Met	Ile	Ile	Gly	Thr	Pro	Tyr	Ala	275	280	285
Asp	Val	Phe	Ala	Ile	Ala	Leu	Glu	Asn	Ala	Gly	Gln	Val	Trp	Ile	Val	290	295	300
Asp	Tyr	Asn	Lys	Glu	Gly	Phe	Pro	Val	Thr	Lys	Ile	Glu	Lys	Val	Gly	305	310	315
Arg	His	Leu	His	Asp	Ala	Phe	Leu	Thr	His	Gly	Gly	Lys	Lys	Leu	Met	325	330	335
Val	Ala	Ser	Tyr	Asp	Asp	Ser	Ile	Val	Ala	Ala	Ile	Asp	Leu	Glu	Lys	340	345	350

Arg Glu Leu Ile Lys Gln Leu Pro Ala Gly Cys Val Pro His Val Gly
 355 360 365
 Gly Gly Ala Ala Val Val Val Asp Gly Arg Thr Leu Gly Phe Gly Thr
 370 375 380
 Asn Phe Gly Asp Cys Asp Lys Met Val Val Ser Val Trp Asp Leu Asp
 385 390 395 400
 Lys Met Glu Val Val Lys Gln Val Pro Val Ser Gly Gly Thr Glu Ser
 405 410 415
 Pro Ala Ala His Ala Asn Ala Pro Tyr Val Ala Val Asp Ile Ile Ser
 420 425 430
 Lys Asp Arg Arg Ala Arg Thr Ile Gln Leu Ile Asp Lys Lys Thr Leu
 435 440 445
 Glu Val Ala Lys Thr Leu Asp Val Gly Gly His Ala Tyr Phe Pro Glu
 450 455 460
 Tyr Ser Ala Asp Gly Lys Phe Leu Tyr Val Ser Ala Gly Tyr Asn Gly
 465 470 475 480
 Asp Glu Val Val Val Tyr Asp Ser Asn Thr Leu Gln Lys Val Ala Thr
 485 490 495
 Val Pro Met Glu Ser Pro Ala Gly Ile Phe Ser Arg Gly Arg Val Lys
 500 505 510
 Tyr Met Thr Arg Gly Leu Ser Pro Asp Glu Met Glu Gln Gly Lys
 515 520 525

Terpenoid genes

<210> 61
 <211> 1860
 <212> DNA
 <213> Methylobionas 16a

<220>
 <223> DXS

<400> 61
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 gcgctgtcca aggaccagct ccagcaactg gctgacgagg tgcgcggcta tctgaccac 120
 acggtcagca ttccggcgcg ccattttgcg gccggcctcg gcaccgtgga actgaccgtg 180
 gccttgcatc atgtgttcaa taccctcgct gatcagttgg tctgggacgt gggccatcag 240
 gcctatccgc acaagattct gaccggtcgc aaggagcgca tgccgaccat tcgcaccctg 300
 ggcgggggtg cagcctttcc ggcgcgggac gagagcgaat acgatgcctt cggcgctcggc 360
 cattccagca cctcgatcag cgcggcactg ggcattggcca ttgcgtcgca gctgcgcggc 420
 gaagacaaga agatggtagc catcatcggc gacggttcca tcaccggcgg catggcctat 480
 gaggcgatga atcatgccgg cgatgtgaat gccaacctgc tggatgatct gaacgacaac 540
 gatatgtcga tctcgccgccc ggtcggggcg atgaacaatt atctgaccaa ggtgtgtcgc 600
 agcaagtttt attcgtcggt gcgggaagag agcaagaaag ctctggccaa gatgccgtcg 660
 gtgtgggaac tggcgcgcaa gaccgaggaa cacgtgaagg gcatgatcgt gcccgggtacc 720
 ttgttcgagg aattgggctt caattatttc ggcccgatcg acggccatga tgtcgagatg 780
 ctggtgtcga ccctggaaaa tctgaaggat ttgaccgggc cggatttctt gcatgtgggtg 840
 accaagaagg gcaaaggcta tgcgccagcc gagaaagacc cgttggccta ccatggcgtg 900

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ccggctttcg atccgaccaa ggattttcctg cccaaggcgg cgcggtcgcc gcatccgacc 960
tataccgagg tggtcggccg ctggctgtgc gacatggcgg ctcaagacga gcgcttgctg 1020
ggcatcacgc cggcgatgcg cgaaggctct ggtttggtgg aattctcaca gaaatttccg 1080
aatcgctatt tcgatgtcgc catcgccgag cagcatgcgg tgaccttggc cgccggccag 1140
gcctgccagg gcgccaagcc ggtggtggcg atttattcca ccttcctgca acgcggttac 1200
gatcagttga tccacgacgt ggccttgacg aacttagata tgctctttgc actggatcgt 1260
gccggcttgg tcggcccggg tggaccgacc catgctggcg cctttgatta cagctacatg 1320
cgctgtattc cgaacatgct gatcatggct ccagccgacg agaacgagtg caggcagatg 1380
ctgaccaccg gcttccaaca ccatggcccg gcttcggtgc gctatccgcg cggcaaaggg 1440
cccggggcgg caatcgatcc gaccctgacc gcgctggaga tcggcaaggc cgaagtcaga 1500
caccacggca gccgcacgc cattctggcc tggggcagca tggtcacgcc tgccgtcgaa 1560
gccggcaagc agctgggcgc gacggtggtg aacatgcgtt tcgtcaagcc gttcgatcaa 1620
gccttggtgc tgggaattggc caggacgcac gatgtgttcg tcaccgtcga ggaaaacgtc 1680
atcgccggcg gcgctggcag tgcgatcaac accttcctgc aggcgcagaa ggtgctgatg 1740
ccggtctgca acatcggcct gcccgaccgc ttcgtcgagc aaggtagtcg cgaggaattg 1800
ctcagcctgg tcggcctcga cagcaagggc atcctcgcca ccatcgaaca gttttgcgct 1860

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<210> 62

<211> 620

<212> PRT

<213> Methylobionas 16a

<220>

<223> Amino acid sequences encoded by DXS

<400> 62

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Met Lys Leu Thr Thr Asp Tyr Pro Leu Leu Lys Asn Ile His Thr Pro
  1                      5                      10                      15

Ala Asp Ile Arg Ala Leu Ser Lys Asp Gln Leu Gln Gln Leu Ala Asp
      20                      25                      30

Glu Val Arg Gly Tyr Leu Thr His Thr Val Ser Ile Ser Gly Gly His
      35                      40                      45

Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr
      50                      55                      60

Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln
      65                      70                      75                      80

Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr
      85                      90                      95

Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser
      100                     105                     110

Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala
      115                     120                     125

Ala Leu Gly Met ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys
      130                     135                     140

Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met ala Tyr
      145                     150                     155                     160

Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile
      165                     170                     175

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Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn
 180 185 190
 Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg
 195 200 205
 Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu
 210 215 220
 Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr
 225 230 235 240
 Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His
 245 250 255
 Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr
 260 265 270
 Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala
 275 280 285
 Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp
 290 295 300
 Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr
 305 310 315 320
 Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met ala Ala Gln Asp
 325 330 335
 Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu
 340 345 350
 Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile
 355 360 365
 Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly
 370 375 380
 Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr
 385 390 395 400
 Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe
 405 410 415
 Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala
 420 425 430
 Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile
 435 440 445
 Met ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly
 450 455 460
 Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly
 465 470 475 480
 Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys
 485 490 495

Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly
500 505 510

Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr
515 520 525

Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu
530 535 540

Glu Leu Ala Arg Thr His Asp Val Phe Val Thr Val Glu Glu Asn Val
545 550 555 560

Ile Ala Gly Gly Ala Gly Ser Ala Ile Asn Thr Phe Leu Gln Ala Gln
565 570 575

Lys Val Leu Met Pro Val Cys Asn Ile Gly Leu Pro Asp Arg Phe Val
580 585 590

Glu Gln Gly Ser Arg Glu Glu Leu Leu Ser Leu Val Gly Leu Asp Ser
595 600 605

Lys Gly Ile Leu Ala Thr Ile Glu Gln Phe Cys Ala
610 615 620

<210> 63

<211> 1182

<212> DNA

<213> Methylomonas 16a

<220>

<223> DXR

<400> 63

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gttgccaggc	atccggataa	atatcaagtc	gttgcgctga	ccgccaacgg	caatatcgac	120
gcattgtatg	aacaatgcct	ggcccaccat	ccggagtatg	cggtgggtgg	catggaaagc	180
aaggtagcag	agttcaaaca	gcgcattgcc	gcttcgccgg	tagcggatat	caaggtcttg	240
tcgggtagcg	aggccttgca	acaggtggcc	acgctggaaa	acgtcgatac	ggtgatggcg	300
gctatcgctg	gcgcggccgg	attggtgccg	accttggccg	cgccaaggc	cggcaaaacc	360
gtgctgttgg	ccaacaagga	agccttggtg	atgtcgggac	aaatcttcat	gcaggccgtc	420
agcgattccg	gcgctgtgtt	gctgccgata	gacagcgagc	acaacgccat	ctttcagtgc	480
atgccggcgg	gttatacgcc	aggccataca	gccaacagg	cgcgccgcac	tttattgacc	540
gcttcgggtg	gcccatttcg	acggacgccg	atagaaacgt	tgtccagcgt	cacgccggat	600
caggccgttg	cccatacctaa	atgggacatg	gggcgcaaga	tttcggtcga	ttccgccacc	660
atgatgaaca	aaggtctcga	actgatcgaa	gcctgcttgt	tggtcaacat	ggagcccgc	720
cagattgaag	tcgtcattca	tccgcagagc	atcattcatt	cgatgggtgga	ctatgtcgat	780
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gcctggccgg	aacgctttga	ctctggtgtg	gcgccgctgg	atattttcga	agtagggcac	900
atggatttcg	aaaaaccgga	cttgaaacgg	tttccttgtc	tgagattggc	ttatgaagcc	960
atcaagtctg	gtggaattat	gccaacggta	ttgaacgcag	ccaatgaaat	tgctgtcgaa	1020
gcgtttttta	atgaagaagt	caaattcact	gacatcgcg	tcatacatga	gcgcagcatg	1080
gccagtttta	aaccggacga	tgccggcagc	ctcgaattgg	ttttgcaggc	cgatcaagat	1140
gcgcgcgagg	tggctagaga	catcatcaag	accttggtag	ct		1182

<210> 64

<211> 394

<212> PRT

<213> Methylomonas 16a

<220>

<223> Amino acid sequences encoded by DXR

<400> 64

Met Lys Gly Ile Cys Ile Leu Gly Ala Thr Gly Ser Ile Gly Val Ser
1 5 10 15
Thr Leu Asp Val Val Ala Arg His Pro Asp Lys Tyr Gln Val Val Ala
20 25 30
Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln Cys Leu Ala
35 40 45
His His Pro Glu Tyr Ala Val Val Val Met Glu Ser Lys Val Ala Glu
50 55 60
Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile Lys Val Leu
65 70 75 80
Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu Asn Val Asp
85 90 95
Thr Val Met ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu
100 105 110
Ala Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn Lys Glu Ala
115 120 125
Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser Asp Ser Gly
130 135 140
Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile Phe Gln Cys
145 150 155 160
Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln Ala Arg Arg
165 170 175
Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr Pro Ile Glu
180 185 190
Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His Pro Lys Trp
195 200 205
Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met Met Asn Lys
210 215 220
Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met Glu Pro Asp
225 230 235 240
Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His Ser Met Val
245 250 255
Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn Pro Asp Met
260 265 270
Arg Thr Pro Ile Ala His Ala Met ala Trp Pro Glu Arg Phe Asp Ser
275 280 285
Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met Asp Phe Glu
290 295 300

Lys Pro Asp Leu Lys Arg Phe Pro Cys Leu Arg Leu Ala Tyr Glu Ala
 305 310 315 320
 Ile Lys Ser Gly Gly Ile Met Pro Thr Val Leu Asn Ala Ala Asn Glu
 325 330 335
 Ile Ala Val Glu Ala Phe Leu Asn Glu Glu Val Lys Phe Thr Asp Ile
 340 345 350
 Ala Val Ile Ile Glu Arg Ser Met ala Gln Phe Lys Pro Asp Asp Ala
 355 360 365
 Gly Ser Leu Glu Leu Val Leu Gln Ala Asp Gln Asp Ala Arg Glu Val
 370 375 380
 Ala Arg Asp Ile Ile Lys Thr Leu Val Ala
 385 390

<210> 65
 <211> 471
 <212> DNA
 <213> Methylomonas 16a

<220>
 <223> ISPF

<400> 65
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 gtgctgcacg cattggccga cgccatcttg ggagccgccg ctttgggcca catcggcaaa 180
 catttcccgg acaccgaccc caatttcaag ggcgccgaca gcaggggtgct actgcgccac 240
 gtgtacggca tcgtcaagga aaaaggctat aaactgggtca acgccgacgt gaccatcatc 300
 gctcaggcgc cgaagatgct gccacacgtg cccggcatgc gcgccaacat tgccgccgat 360
 ctggaaaccg atgtcgattt cattaatgta aaagccacga cgaccgagaa actgggcttt 420
 gagggccgta aggaaggcat cgccgtgcag gctgtggtgt tgatagaacg c 471

<210> 66
 <211> 157
 <212> PRT
 <213> Methylomonas 16a

<220>
 <223> Amino acid sequences encoded by ISPF

<400> 66
 Met Ile Arg Val Gly Met Gly Tyr Asp Val His Arg Phe Asn Asp Gly
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 Asp His Ile Ile Leu Gly Gly Val Lys Ile Pro Tyr Glu Lys Gly Leu
 20 25 30
 Glu Ala His Ser Asp Gly Asp Val Val Leu His Ala Leu Ala Asp Ala
 35 40 45
 Ile Leu Gly Ala Ala Ala Leu Gly Asp Ile Gly Lys His Phe Pro Asp
 50 55 60

Thr Asp Pro Asn Phe Lys Gly Ala Asp Ser Arg Val Leu Leu Arg His
 65 70 75 80
 Val Tyr Gly Ile Val Lys Glu Lys Gly Tyr Lys Leu Val Asn Ala Asp
 85 90 95
 Val Thr Ile Ile Ala Gln Ala Pro Lys Met Leu Pro His Val Pro Gly
 100 105 110
 Met Arg Ala Asn Ile Ala Ala Asp Leu Glu Thr Asp Val Asp Phe Ile
 115 120 125
 Asn Val Lys Ala Thr Thr Thr Glu Lys Leu Gly Phe Glu Gly Arg Lys
 130 135 140
 Glu Gly Ile Ala Val Gln Ala Val Val Leu Ile Glu Arg
 145 150 155

<210> 67
 <211> 693
 <212> DNA
 <213> Methylobionas 16a

<220>
 <223> ISPD

<400> 67
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 caagccgatc gcccacaaaca atattttaccg cttgcccggta aaacgggtcat cgaacacaca 120
 ctgactcgac tacttgagtc cgacgccttc caaaaagttg cgggtggcgat ttccgtcgaa 180
 gacccttatt ggccctgaact gtccatagcc aaacacccccg acatcatcac cgcgcctggc 240
 ggcaaggaac gcgcgcgactc ggtgctgtct gcactgaagg ctttagaaga tatagccagc 300
 gaaaatgatt ggggtgctggt acacgacgcc gccgcgccct gcttgacggg cagcgacatc 360
 caccttcaaa tcgatacctt aaaaaatgac ccggctcggcg gcatacctggc cttgagttcg 420
 cagcacacat tgaacacgt ggatgggtgac acgatcaccg caaccataga cagaaagcac 480
 gtctggcgcg ccttgacgcc gcaaatgttc aaatacggca tgttgcgcca cgcgttgcaa 540
 cgaaccgaag gcaatccggc cgtcaccgac gaagccagtg cgctggaact tttgggccat 600
 aaacccaaaa tcgtggaagg ccgcccggac aacatcaaaa tcacccgccc ggaagatttg 660
 gccctggcac aattttatat ggagcaacaa gca 693

<210> 68
 <211> 231
 <212> PRT
 <213> Methylobionas 16a

<220>
 <223> Amino acid sequences encoded by ISPD

<400> 68
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 1 5 10 15
 Gly Lys Arg Met Gln Ala Asp Arg Pro Lys Gln Tyr Leu Pro Leu Ala
 20 25 30
 Gly Lys Thr Val Ile Glu His Thr Leu Thr Arg Leu Leu Glu Ser Asp
 35 40 45

Ala Phe Gln Lys Val Ala Val Ala Ile Ser Val Glu Asp Pro Tyr Trp
50 55 60

Pro Glu Leu Ser Ile Ala Lys His Pro Asp Ile Ile Thr Ala Pro Gly
65 70 75 80

Gly Lys Glu Arg Ala Asp Ser Val Leu Ser Ala Leu Lys Ala Leu Glu
85 90 95

Asp Ile Ala Ser Glu Asn Asp Trp Val Leu Val His Asp Ala Ala Arg
100 105 110

Pro Cys Leu Thr Gly Ser Asp Ile His Leu Gln Ile Asp Thr Leu Lys
115 120 125

Asn Asp Pro Val Gly Gly Ile Leu Ala Leu Ser Ser His Asp Thr Leu
130 135 140

Lys His Val Asp Gly Asp Thr Ile Thr Ala Thr Ile Asp Arg Lys His
145 150 155 160

Val Trp Arg Ala Leu Thr Pro Gln Met Phe Lys Tyr Gly Met Leu Arg
165 170 175

Asp Ala Leu Gln Arg Thr Glu Gly Asn Pro Ala Val Thr Asp Glu Ala
180 185 190

Ser Ala Leu Glu Leu Leu Gly His Lys Pro Lys Ile Val Glu Gly Arg
195 200 205

Pro Asp Asn Ile Lys Ile Thr Arg Pro Glu Asp Leu Ala Leu Ala Gln
210 215 220

Phe Tyr Met Glu Gln Gln Ala
225 230

210> 69
<211> 1632
<212> DNA
<213> Methylobionas 16a

<220>
<223> PYRG

<400> 69
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gcctcctccc tggcggcgat tctggaagac cgcggcctca aagtcactat cacaaaactc 120
gatccctaca tcaacgtcga ccccggcacc atgagcccgt ttcaacacgg cgaggtgttc 180
gtgaccgaag acggtgccga aaccgatttg gaccttgcc attacgaacg gtttttgaaa 240
accacgatga ccaagaaaaa caacttcacc accggtcagg ttacgagca ggtattacgc 300
aacgagcgca aaggtgatta tcttggcgcg accgtgcaag tcattccaca tatcaccgac 360
gaaatcaaac gccgggtgta tgaaagcgcc gaagggaag atgtggcatt gatcgaagtc 420
ggcggcacgg tggcgacat cgaatcgta ccgtttctgg aaaccatacg ccagatgggc 480
gtggaactgg gtggtgaccg cgccttggtt attcatttga cgctgggtgc ttacatcaaa 540
tcggccggcg aactgaaaac caagcccacc cagcattcgg tcaaagaact gcgcaccatc 600
gggattcagc cggacatttt gatctgtcgt tcagaacaac cgatcccggc cagtgaacgc 660
cgcaagatcg cgctattttac caatgtcgcc gaaaaggcgg tgatttccgc gatcgatgcc 720
gacaccattt accgcatttc gctattgctg cgcaacaag gcctggacga cctgggtggc 780
gatcagttgc gcctggacgt accagcggcg gatttatcgg cctgggaaaa ggtcgtcgat 840

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aaggtgcaaa tcagctacat cgactccgaa accatagaag ccgaaggcac cgccaaattg 1020
aaaaacgtcg atgcgatcct ggtgccgggt ggtttcggcg aacgcggcgt ggaaggcaag 1080
atttctaccg tgcgttttgc ccgcgagaac aaaatcccgt atttgggcat ttgcttgggc 1140
atgcaatcgg cggtaatcga attcgcccgc aacgtgggtg gcctggaagg cgcgcacagc 1200
accgaattcc tgccgaaatc gccacaccct gtgatcggct tgatcaccga atggatggac 1260
gaagccggcg aactggtcac acgcgacgaa gattccgacg tgggcggcac gatgcgtctg 1320
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gtcatcaccg agcgtcaccg ccaccgctac gaattcaaca atcaatattt aaaacaactg 1440
gaagccggcg gcatgaaatt ttccggtaaa tcgctggacg gccgcctggg ggagatcatc 1500
gagctacccg aacacccttg gttcctggcc tgccagttcc atcccgaatt cacctcgacg 1560
ccgcgtaacg gccacgccct attttcgggc ttcgtcgaag cggccgcca acacaaaaca 1620
caaggcacag ca                                     1632

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<210> 70

<211> 544

<212> PRT

<213> Methylomonas 16a

<220>

<223> Amino acid sequences encoded by ORF6 - PYRG

<400> 70

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Met Thr Lys Phe Ile Phe Ile Thr Gly Gly Val Val Ser Ser Leu Gly
 1           5           10           15

Lys Gly Ile Ala Ala Ser Ser Leu Ala Ala Ile Leu Glu Asp Arg Gly
          20           25           30

Leu Lys Val Thr Ile Thr Lys Leu Asp Pro Tyr Ile Asn Val Asp Pro
 35           40           45

Gly Thr Met Ser Pro Phe Gln His Gly Glu Val Phe Val Thr Glu Asp
 50           55           60

Gly Ala Glu Thr Asp Leu Asp Leu Gly His Tyr Glu Arg Phe Leu Lys
 65           70           75           80

Thr Thr Met Thr Lys Lys Asn Asn Phe Thr Thr Gly Gln Val Tyr Glu
          85           90           95

Gln Val Leu Arg Asn Glu Arg Lys Gly Asp Tyr Leu Gly Ala Thr Val
          100          105          110

Gln Val Ile Pro His Ile Thr Asp Glu Ile Lys Arg Arg Val Tyr Glu
          115          120          125

Ser Ala Glu Gly Lys Asp Val Ala Leu Ile Glu Val Gly Gly Thr Val
          130          135          140

Gly Asp Ile Glu Ser Leu Pro Phe Leu Glu Thr Ile Arg Gln Met Gly
          145          150          155          160

Val Glu Leu Gly Arg Asp Arg Ala Leu Phe Ile His Leu Thr Leu Val
          165          170          175

Pro Tyr Ile Lys Ser Ala Gly Glu Leu Lys Thr Lys Pro Thr Gln His
          180          185          190

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Ser	Val	Lys	Glu	Leu	Arg	Thr	Ile	Gly	Ile	Gln	Pro	Asp	Ile	Leu	Ile	195	200	205	
Cys	Arg	Ser	Glu	Gln	Pro	Ile	Pro	Ala	Ser	Glu	Arg	Arg	Lys	Ile	Ala	210	215	220	
Leu	Phe	Thr	Asn	Val	Ala	Glu	Lys	Ala	Val	Ile	Ser	Ala	Ile	Asp	Ala	225	230	235	240
Asp	Thr	Ile	Tyr	Arg	Ile	Pro	Leu	Leu	Leu	Arg	Glu	Gln	Gly	Leu	Asp	245	250	255	
Asp	Leu	Val	Val	Asp	Gln	Leu	Arg	Leu	Asp	Val	Pro	Ala	Ala	Asp	Leu	260	265	270	
Ser	Ala	Trp	Glu	Lys	Val	Val	Asp	Gly	Leu	Thr	His	Pro	Thr	Asp	Glu	275	280	285	
Val	Ser	Ile	Ala	Ile	Val	Gly	Lys	Tyr	Val	Asp	His	Thr	Asp	Ala	Tyr	290	295	300	
Lys	Ser	Leu	Asn	Glu	Ala	Leu	Ile	His	Ala	Gly	Ile	His	Thr	Arg	His	305	310	315	320
Lys	Val	Gln	Ile	Ser	Tyr	Ile	Asp	Ser	Glu	Thr	Ile	Glu	Ala	Glu	Gly	325	330	335	
Thr	Ala	Lys	Leu	Lys	Asn	Val	Asp	Ala	Ile	Leu	Val	Pro	Gly	Gly	Phe	340	345	350	
Gly	Glu	Arg	Gly	Val	Glu	Gly	Lys	Ile	Ser	Thr	Val	Arg	Phe	Ala	Arg	355	360	365	
Glu	Asn	Lys	Ile	Pro	Tyr	Leu	Gly	Ile	Cys	Leu	Gly	Met	Gln	Ser	Ala	370	375	380	
Val	Ile	Glu	Phe	Ala	Arg	Asn	Val	Val	Gly	Leu	Glu	Gly	Ala	His	Ser	385	390	395	400
Thr	Glu	Phe	Leu	Pro	Lys	Ser	Pro	His	Pro	Val	Ile	Gly	Leu	Ile	Thr	405	410	415	
Glu	Trp	Met	Asp	Glu	Ala	Gly	Glu	Leu	Val	Thr	Arg	Asp	Glu	Asp	Ser	420	425	430	
Asp	Leu	Gly	Gly	Thr	Met	Arg	Leu	Gly	Ala	Gln	Lys	Cys	Arg	Leu	Lys	435	440	445	
Ala	Asp	Ser	Leu	Ala	Phe	Gln	Leu	Tyr	Gln	Lys	Asp	Val	Ile	Thr	Glu	450	455	460	
Arg	His	Arg	His	Arg	Tyr	Glu	Phe	Asn	Asn	Gln	Tyr	Leu	Lys	Gln	Leu	465	470	475	480
Glu	Ala	Ala	Gly	Met	Lys	Phe	Ser	Gly	Lys	Ser	Leu	Asp	Gly	Arg	Leu	485	490	495	
Val	Glu	Ile	Ile	Glu	Leu	Pro	Glu	His	Pro	Trp	Phe	Leu	Ala	Cys	Gln	500	505	510	

Phe His Pro Glu Phe Thr Ser Thr Pro Arg Asn Gly His Ala Leu Phe
515 520 525

Ser Gly Phe Val Glu Ala Ala Ala Lys His Lys Thr Gln Gly Thr Ala
530 535 540

<210> 71
<211> 891
<212> DNA
<213> Methylobionas 16a

<220>
<223> ORF7 ISPa

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gcccgctctgc ctgccgaaaa catactgcca caaaccttgc atcaggccat gcgctattcc 120
gtattgaacg gcggcaaacg caccgcggcc ttgttgactt atgcgaccg tcaggctttg 180
ggcttgccgg aaaacgtgct ggatgcgccc gcttgcgccg tagaattcat ccatgtgtat 240
tcgctgattc acgacgatct gccggccatg gacaacgat atctgcgccc cggcaaaccg 300
acctgtcaca aggtttacga cgaggccacc gccatttttg ccggcgacgc actgcaggcg 360
ctggcctttg aagttctggc caacgacccc ggcatcaccg tcgatgcccc ggctcgctg 420
aaaatgatca cggctttgac ccgcgccagc ggctctcaag gcatgggtggg cggctcaagcc 480
atcgatctcg gctccgctcg ccgcaaattg acgctgccgg aactcgaaaa catgcatatc 540
cacaagactg gcgccctgat ccgcgccagc gtcaatcttg cggcattatc caaacccgat 600
ctggatactt gcgtcgccaa gaaactggat cactatgcca aatgcatagg cttgtcgttc 660
caggtcaaag acgacattct cgacatcgaa gccgacaccg cgacactcgg caagactcag 720
ggcaaggaca tcgataacga caaacgcacc taccctgcgc tattgggcat ggctggcgcc 780
aaacaaaaag cccaggaatt gcacgaacaa gcagtcgaaa gcttaacggg atttggcagc 840
gaagccgacc tgctgcgcga actatcgctt tacatcatcg agcgcacgca c 891

<210> 72
<211> 297
<212> PRT
<213> Methylobionas 16a

<220>
<223> Amino acid sequences encoded by ORF7 - ISPa

<400> 72
Met Ser Lys Leu Lys Ala Tyr Leu Thr Val Cys Gln Glu Arg Val Glu
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Arg Ala Leu Asp Ala Arg Leu Pro Ala Glu Asn Ile Leu Pro Gln Thr
20 25 30
Leu His Gln Ala Met Arg Tyr Ser Val Leu Asn Gly Gly Lys Arg Thr
35 40 45
Arg Pro Leu Leu Thr Tyr Ala Thr Gly Gln Ala Leu Gly Leu Pro Glu
50 55 60
Asn Val Leu Asp Ala Pro Ala Cys Ala Val Glu Phe Ile His Val Tyr
65 70 75 80
Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp Leu Arg
85 90 95
Arg Gly Lys Pro Thr Cys His Lys Ala Tyr Asp Glu Ala Thr Ala Ile
100 105 110

Leu Ala Gly Asp Ala Leu Gln Ala Leu Ala Phe Glu Val Leu Ala Asn
 115 120 125
 Asp Pro Gly Ile Thr Val Asp Ala Pro Ala Arg Leu Lys Met Ile Thr
 130 135 140
 Ala Leu Thr Arg Ala Ser Gly Ser Gln Gly Met Val Gly Gly Gln Ala
 145 150 155 160
 Ile Asp Leu Gly Ser Val Gly Arg Lys Leu Thr Leu Pro Glu Leu Glu
 165 170 175
 Asn Met His Ile His Lys Thr Gly Ala Leu Ile Arg Ala Ser Val Asn
 180 185 190
 Leu Ala Ala Leu Ser Lys Pro Asp Leu Asp Thr Cys Val Ala Lys Lys
 195 200 205
 Leu Asp His Tyr Ala Lys Cys Ile Gly Leu Ser Phe Gln Val Lys Asp
 210 215 220
 Asp Ile Leu Asp Ile Glu Ala Asp Thr Ala Thr Leu Gly Lys Thr Gln
 225 230 235 240
 Gly Lys Asp Ile Asp Asn Asp Lys Pro Thr Tyr Pro Ala Leu Leu Gly
 245 250 255
 Met ala Gly Ala Lys Gln Lys Ala Gln Glu Leu His Glu Gln Ala Val
 260 265 270
 Glu Ser Leu Thr Gly Phe Gly Ser Glu Ala Asp Leu Leu Arg Glu Leu
 275 280 285
 Ser Leu Tyr Ile Ile Glu Arg Thr His
 290 295

<210> 73

<211> 855

<212> DNA

<213> *Methylomonas* 16a

<220>

<223> ISPE

<400> 73

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ctcgatctat gcgattgggt gacgtttcat ccggttgatg atggccgcgt gacgctgcga 180
aatccaatct ccggcggttc agagcaggat gacttgactg ttcgggcggc taatttggtg 240
aagtctcata ccggtgtgtg gcgcggagtt tgtatcgata tcgagaaaaa tctgcctatg 300
ggtggtgggt tgggtggtgg aagttccgat gctgctacaa ccttggtagt tctaaatcgg 360
ctttggggct tgggcttgct gaagcgtgag ttgatggatt tgggcttgag gcttggtgcc 420
gatgtgcctg tgtttgtgtt tggttgttcg gcctggggcg aagggtgtgag cgaggatttg 480
caggcaataa cgttgccgga acaatggttt gtcatcatta aaccggattg ccatgtgaat 540
actggagaaa ttttttctgc agaaaatttg acaaggaata gtgcagtcgt tacaatgagc 600
gactttcttg caggggataa tcggaatgat tgttcggaag tggtttgcaa gttatatcga 660
ccggtgaaag atgcaatcga tgcgttgta tgctatgcgg aagcgagatt gacggggacc 720
ggtgcatgtg tgttcgctca gttttgtaac aaggaagatg ctgagagtgc gttagaagga 780
  
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ttgaaagatc ggtggctggt gttcttggct aaaggcttga atcagttctgc gctctacaag 840
aaattagaac aggga 855

<210> 74
<211> 285
<212> PRT
<213> Methylomonas 16a

<220>
<223> Amino acid sequences encoded by ISPE

<400> 74
Met Asp Tyr Ala Ala Gly Trp Gly Glu Arg Trp Pro Ala Pro Ala Lys
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Leu Asn Leu Met Leu Arg Ile Thr Gly Arg Arg Pro Asp Gly Tyr His
20 25 30
Leu Leu Gln Thr Val Phe Gln Met Leu Asp Leu Cys Asp Trp Leu Thr
35 40 45
Phe His Pro Val Asp Asp Gly Arg Val Thr Leu Arg Asn Pro Ile Ser
50 55 60
Gly Val Pro Glu Gln Asp Asp Leu Thr Val Arg Ala Ala Asn Leu Leu
65 70 75 80
Lys Ser His Thr Gly Cys Val Arg Gly Val Cys Ile Asp Ile Glu Lys
85 90 95
Asn Leu Pro Met Gly Gly Gly Leu Gly Gly Gly Ser Ser Asp Ala Ala
100 105 110
Thr Thr Leu Val Val Leu Asn Arg Leu Trp Gly Leu Gly Leu Ser Lys
115 120 125
Arg Glu Leu Met Asp Leu Gly Leu Arg Leu Gly Ala Asp Val Pro Val
130 135 140
Phe Val Phe Gly Cys Ser Ala Trp Gly Glu Gly Val Ser Glu Asp Leu
145 150 155 160
Gln Ala Ile Thr Leu Pro Glu Gln Trp Phe Val Ile Ile Lys Pro Asp
165 170 175
Cys His Val Asn Thr Gly Glu Ile Phe Ser Ala Glu Asn Leu Thr Arg
180 185 190
Asn Ser Ala Val Val Thr Met Ser Asp Phe Leu Ala Gly Asp Asn Arg
195 200 205
Asn Asp Cys Ser Glu Val Val Cys Lys Leu Tyr Arg Pro Val Lys Asp
210 215 220
Ala Ile Asp Ala Leu Leu Cys Tyr Ala Glu Ala Arg Leu Thr Gly Thr
225 230 235 240
Gly Ala Cys Val Phe Ala Gln Phe Cys Asn Lys Glu Asp Ala Glu Ser
245 250 255

Ala Leu Glu Gly Leu Lys Asp Arg Trp Leu Val Phe Leu Ala Lys Gly
 260 265 270

Leu Asn Gln Ser Ala Leu Tyr Lys Lys Leu Glu Gln Gly
 275 280 285

<210> 75
 <211> 1533
 <212> DNA
 <213> Methylobionas 16a

<220>
 <223> CRTN1

<400> 75
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 ggccgcaacc gcccgatcaa catgaacggc tttaccttcg ataccgggtcc gacattcttg 180
 ttgatgaaag gcgtgctgga cgaaatgttc gaactgtgag agcgccgtag cgaggattat 240
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 gtctattccg accgcgagaa catgcgcgcc gaattgcaac gggatttcga cgaaggcacg 360
 gacggctacg aacagttcat ggaacaggaa cgcaaacgct tcaacgcgct gtatccctgc 420
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 aaaatgcgcc tggccttttg ctttcagtcc aagtatctgg gcatgtcgcc gtgggaatgc 600
 ccggcactgt ttacgatgct gccctatctg gagcacgaat acggcattta tcacgtcaaa 660
 ggccggcctga accgcatcgc ggccggcgatg gcgcaagtga tcgcggaaaa cggcgccgaa 720
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 aagcagcgcg agtattcctg ttccgacctc atgctgtatc tgggtttgga caagatttac 960
 gatctgccc accataccat cgtgtttgcc aaggattaca ccaccaatat ccgcaacatt 1020
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 aacgacagcg gcctggactg gcaggcgcat tgccaaaacg tgcggaaca ggtgttgga 1200
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 atcagcgccg aaacctggga aacggacgaa cacgtttaca agggcgccac tttcagtttg 1320
 tcgcacaagt tcagccaaat gctgtactgg cggccgcaca accgtttcga ggaactggcc 1380
 aattgctatc tggtcggcgg cggcacgcat cccggtagcg gtttgccgac catctacgaa 1440
 tcggcgcgga tttcgcccaa gctgatttcc cagaaacatc gggtagaggt caaggacata 1500
 gcacacagcg cctggctgaa aaaagccaaa gcc 1533

<210> 76
 <211> 511
 <212> PRT
 <213> Methylobionas 16a

<220>
 <223> Amino acid sequences encoded by CRTN1
 <400> 76

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 20 25 30

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		35					40					45				
Asn	Gly	Phe	Thr	Phe	Asp	Thr	Gly	Pro	Thr	Phe	Leu	Leu	Met	Lys	Gly	
	50					55					60					
Val	Leu	Asp	Glu	Met	Phe	Glu	Leu	Cys	Glu	Arg	Arg	Ser	Glu	Asp	Tyr	
	65				70					75					80	
Leu	Glu	Phe	Leu	Pro	Leu	Ser	Pro	Met	Tyr	Arg	Leu	Leu	Tyr	Asp	Asp	
				85					90					95		
Arg	Asp	Ile	Phe	Val	Tyr	Ser	Asp	Arg	Glu	Asn	Met	Arg	Ala	Glu	Leu	
			100					105					110			
Gln	Arg	Val	Phe	Asp	Glu	Gly	Thr	Asp	Gly	Tyr	Glu	Gln	Phe	Met	Glu	
		115					120					125				
Gln	Glu	Arg	Lys	Arg	Phe	Asn	Ala	Leu	Tyr	Pro	Cys	Ile	Thr	Arg	Asp	
	130					135					140					
Tyr	Ser	Ser	Leu	Lys	Ser	Phe	Leu	Ser	Leu	Asp	Leu	Ile	Lys	Ala	Leu	
	145				150					155					160	
Pro	Trp	Leu	Ala	Phe	Pro	Lys	Ser	Val	Phe	Asn	Asn	Leu	Gly	Gln	Tyr	
				165					170					175		
Phe	Asn	Gln	Glu	Lys	Met	Arg	Leu	Ala	Phe	Cys	Phe	Gln	Ser	Lys	Tyr	
			180					185					190			
Leu	Gly	Met	Ser	Pro	Trp	Glu	Cys	Pro	Ala	Leu	Phe	Thr	Met	Leu	Pro	
		195					200					205				
Tyr	Leu	Glu	His	Glu	Tyr	Gly	Ile	Tyr	His	Val	Lys	Gly	Gly	Leu	Asn	
	210					215					220					
Arg	Ile	Ala	Ala	Ala	Met	ala	Gln	Val	Ile	Ala	Glu	Asn	Gly	Gly	Glu	
	225				230					235					240	
Ile	His	Leu	Asn	Ser	Glu	Ile	Glu	Ser	Leu	Ile	Ile	Glu	Asn	Gly	Ala	
				245					250					255		
Ala	Lys	Gly	Val	Lys	Leu	Gln	His	Gly	Ala	Glu	Leu	Arg	Gly	Asp	Glu	
			260					265					270			
Val	Ile	Ile	Asn	Ala	Asp	Phe	Ala	His	Ala	Met	Thr	His	Leu	Val	Lys	
		275					280					285				
Pro	Gly	Val	Leu	Lys	Lys	Tyr	Thr	Pro	Glu	Asn	Leu	Lys	Gln	Arg	Glu	
	290					295					300					
Tyr	Ser	Cys	Ser	Thr	Phe	Met	Leu	Tyr	Leu	Gly	Leu	Asp	Lys	Ile	Tyr	
	305				310					315					320	
Asp	Leu	Pro	His	His	Thr	Ile	Val	Phe	Ala	Lys	Asp	Tyr	Thr	Thr	Asn	
				325					330					335		
Ile	Arg	Asn	Ile	Phe	Asp	Asn	Lys	Thr	Leu	Thr	Asp	Asp	Phe	Ser	Phe	
			340					345					350			

Tyr Val Gln Asn Ala Ser Ala Ser Asp Asp Ser Leu Ala Pro Ala Gly
 355 360 365
 Lys Ser Ala Leu Tyr Val Leu Val Pro Met Pro Asn Asn Asp Ser Gly
 370 375 380
 Leu Asp Trp Gln Ala His Cys Gln Asn Val Arg Glu Gln Val Leu Asp
 385 390 395 400
 Thr Leu Gly Ala Arg Leu Gly Leu Ser Asp Ile Arg Ala His Ile Glu
 405 410 415
 Cys Glu Lys Ile Ile Thr Pro Gln Thr Trp Glu Thr Asp Glu His Val
 420 425 430
 Tyr Lys Gly Ala Thr Phe Ser Leu Ser His Lys Phe Ser Gln Met Leu
 435 440 445
 Tyr Trp Arg Pro His Asn Arg Phe Glu Glu Leu Ala Asn Cys Tyr Leu
 450 455 460
 Val Gly Gly Gly Thr His Pro Gly Ser Gly Leu Pro Thr Ile Tyr Glu
 465 470 475 480
 Ser Ala Arg Ile Ser Ala Lys Leu Ile Ser Gln Lys His Arg Val Arg
 485 490 495
 Phe Lys Asp Ile Ala His Ser Ala Trp Leu Lys Lys Ala Lys Ala
 500 505 510

<210> 77

<211> 1491

<212> DNA

<213> Methylobionas 16a

<220>

<223> CRTN2

<400> 77

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gtcggcggca	agctcaacat	catgaccaa	gacggcttta	ccttcgatct	ggggccgtcc	180
atcttgacga	tgccgcacat	ctttgaggcc	ttgttcacag	gggcccggca	aaacatggcc	240
gattacgtgc	aaatccagaa	agtcgaaccg	cactggcgca	atttcttcga	ggacggtagc	300
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ggcacttacg	cgcaattcca	gcgctttctg	gactattcga	aaaacctctg	cacggaaacc	420
gaagccgggt	acttcgcca	gggcctggac	ggcttttggg	atttactcaa	gttttacggc	480
ccgctccgca	gcctgctgag	tttcgacgtc	ttccgcagca	tgaccagggg	cgtgcgccgc	540
tttatttcgc	atcccaagtt	ggtcgaaatc	ctgaattact	tcacaaaata	cgtcgggtcc	600
tcgccttacg	atgcgcccgc	cttgatgaac	ctgctgcctt	acattcaata	tcattacggc	660
ctgtggttacg	tgaaaggcgg	catgtatggc	atggcgccag	ccatggaaaa	actggccgtg	720
gaattggggc	tcgagattcg	tttagatgcc	gaggtgtcgg	aaatccaaaa	acaggacggc	780
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<211> 497

<212> PRT

<213> Methylomonas 16a

<220>

<223> Amino acid sequences encoded by CRTN2

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 355 360 365
 Pro Ala Gly Cys Glu Ile Ile Lys Ile Leu Pro His Ile Pro His Leu
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 450 455 460
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<210> 79

<211> 1455

<212> DNA

<213> METHYLOMONAS SP.

<400> 79

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<210> 80

<211> 485

<212> PRT

<213> METHYLOMONAS SP.

<400> 80

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Leu His Arg Arg Arg Cys Phe Leu Ile Glu Asp Leu Arg Lys Met Thr
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Ala Gly Met Thr Cys Ser Arg Leu Pro Glu Asp Leu Asn Tyr Lys Phe
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Ser Ser Asn Arg Gly Gly Asn Met Lys Ile Ile Lys Asp Arg Val Ala
      65              70              75              80

Lys Leu Ser Phe Val Ala Leu Leu Ile Thr Met Thr Ala Ala Met Phe
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Tyr Ala Pro Thr Ala Ser Ala His Gly Glu Lys Ser Gln Ala Ala Phe
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Met Arg Met Arg Thr Ile His Trp Phe Asp Leu Asn Trp Ser Ala Asp
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Glu Val Ala Val Asn Asp Thr Met Thr Ile Ser Gly Lys Phe His Val
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Tyr	Glu	Phe	Lys	Val	Leu	Leu	Lys	Ala	Arg	Arg	Pro	Gly	Asp	Trp	His	195	200	205	
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Leu	Ser	Val	Ser	Asp	Asn	Ser	Pro	Ile	Ala	Pro	Gly	Glu	Thr	Arg	Thr	420	425	430	
Val	Glu	Val	Thr	Ala	Ser	Asp	Ala	Ala	Trp	Glu	Val	Tyr	Arg	Leu	Ala	435	440	445	
Asp	Leu	Ile	Tyr	Asp	Pro	Asp	Ser	Arg	Phe	Ala	Gly	Leu	Met	Phe	Phe	450	455	460	

Trp Asp Glu Asn Gly Asn Arg Gln Met Thr Met Val Asp Ala Pro Leu
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